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SEQUENCE LISTING

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Yoshida, Carolina Andrea
Zanma, Akira
Kobayashi, Shinji
Yamana, Kei

<120> BONE AND/OR JOINT-DISEASE-ASSOCIATES GENES

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<151> 2004-10-20

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gtg acc aag aag gct aag aaa gag act tca tcc agt gac agc agt gag			354
Val Thr Lys Lys Ala Lys Lys Glu Thr Ser Ser Ser Asp Ser Ser Glu			
75	80	85	
gac agc agt gag gac gag gac aaa aaa gcc cag gga ctt ccc aca cag			402
Asp Ser Ser Glu Asp Glu Asp Lys Lys Ala Gln Gly Leu Pro Thr Gln			
90	95	100	105
aag gct gcc gca cag gtc aag cga gcc agt gtg cct cag cat gct gga			450
Lys Ala Ala Ala Gln Val Lys Arg Ala Ser Val Pro Gln His Ala Gly			
110	115	120	
aag gca gca gcc aaa gct tca gag agc agc agt agt gaa gaa tcc agt			498
Lys Ala Ala Ala Lys Ala Ser Glu Ser Ser Ser Glu Glu Ser Ser			
125	130	135	
gag gaa gag gaa gag gac aaa aag aaa aag cct gtc cag aag gca gct			546
Glu Glu Glu Glu Asp Lys Lys Lys Pro Val Gln Lys Ala Ala			
140	145	150	
aag ccc caa gcc aag gca gtc aga cct cct gcg aag aag gca gag agc			594
Lys Pro Gln Ala Lys Ala Val Arg Pro Pro Ala Lys Lys Ala Glu Ser			
155	160	165	
tct gag tcg gac tca gac tcg gat tcg gac tcc agc tca gag gaa gaa			642
Ser Glu Ser Asp Ser Asp Ser Asp Ser Ser Ser Glu Glu Glu			
170	175	180	185
aca cca cag acc cag aag cca aag gca gct gtg gca gca aaa gct cag			690
Thr Pro Gln Thr Gln Lys Pro Lys Ala Ala Val Ala Ala Lys Ala Gln			
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act aaa gcc gaa gcc aaa cca ggt aca cca gcg aaa gca cag cct aag			738
Thr Lys Ala Glu Ala Lys Pro Gly Thr Pro Ala Lys Ala Gln Pro Lys			
205	210	215	
gta gcc aat ggc aaa gca gcc gcc agc agc agc agc agc agc agc agc			786
Val Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser			
220	225	230	
gat gac tca gag gaa gag aag aag gca gct gca cct ccc aag aag act			834
Asp Asp Ser Glu Glu Lys Lys Ala Ala Pro Pro Lys Lys Thr			
235	240	245	
gta cca aaa aag caa gtc gtg gcc aag gcc cca gtg aaa gta gct gcc			882
Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Val Ala Ala			
250	255	260	265
gcc ccc acc cag aag agc tcc agc agt gag gat tct tcc agt gaa gag			930
Ala Pro Thr Gln Lys Ser Ser Ser Glu Asp Ser Ser Glu Glu			
270	275	280	
gag gag gga cag aga caa ccc atg aag aaa aaa gca ggt ccc tac agt			978
Glu Glu Gly Gln Arg Gln Pro Met Lys Lys Lys Ala Gly Pro Tyr Ser			
285	290	295	
tca gtt cca cca ccc tct gtt cct tta cca aag aag tcc ccg gga acc			1026

Ser Val Pro Pro Ser Val Pro Leu Pro Lys Lys Ser Pro Gly Thr			
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cag gct cca aag aaa gct gct gcg cag aca cag cct gca gac agc agt			1074
Gln Ala Pro Lys Lys Ala Ala Gln Thr Gln Pro Ala Asp Ser Ser			
315	320	325	
gac gac agc agt gac gat tct gat tca agt tct gag gaa gag aaa aaa			1122
Asp Asp Ser Ser Asp Asp Ser Ser Ser Glu Glu Glu Lys Lys			
330	335	340	345
cct cca gct aag acg gtc gtc tcc aag aca ccc gcc aaa gca gct cca			1170
Pro Pro Ala Lys Thr Val Val Ser Lys Thr Pro Ala Lys Ala Ala Pro			
350	355	360	
gtg aag aag aaa gca gaa agc tct tca gac agc tcg gat tct gac agt			1218
Val Lys Lys Ala Glu Ser Ser Asp Ser Ser Asp Ser Asp Ser Asp Ser			
365	370	375	
tct gag gat gaa gct cct gcc aag cca gtc agt aca acc aag agt ccc			1266
Ser Glu Asp Glu Ala Pro Ala Lys Pro Val Ser Thr Thr Lys Ser Pro			
380	385	390	
aag cca gct gtc act ccg aag cca tct gca gca aag gca gtg aca act			1314
Lys Pro Ala Val Thr Pro Lys Pro Ser Ala Ala Lys Ala Val Thr Thr			
395	400	405	
cct aag caa cct gca ggc agt aac cag aaa cct cag agc agg aag gct			1362
Pro Lys Gln Pro Ala Gly Ser Asn Gln Lys Pro Gln Ser Arg Lys Ala			
410	415	420	425
gac agc agc tcc agc gag gag gaa agc agc tcc agc gag gag gag gag			1410
Asp Ser Ser Ser Ser Glu Glu Ser Ser Ser Glu Glu Glu Glu Glu			
430	435	440	
gcc tcc aag aaa agt gcc aca acc ccc aag gcc aag gtg act gct aaa			1458
Ala Ser Lys Lys Ser Ala Thr Thr Pro Lys Ala Lys Val Thr Ala Lys			
445	450	455	
gca gca ccc gcc aaa cag gcc cct cag gct gct ggg gac agc agc tct			1506
Ala Ala Pro Ala Lys Gln Ala Pro Gln Ala Ala Gly Asp Ser Ser Ser			
460	465	470	
gac tca gat agt tcc agc agt gaa gag gag gag aag act cct aag ccc			1554
Asp Ser Asp Ser Ser Ser Glu Glu Glu Glu Lys Thr Pro Lys Pro			
475	480	485	
cca gct aag aag aag gca gca ggt gga gcc gtt tct aca cca gcc cct			1602
Pro Ala Lys Lys Ala Ala Gly Gly Ala Val Ser Thr Pro Ala Pro			
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Gly Lys Lys Ala Glu Ala Lys Ser Ser Ser Ser Ser Ser Ser Ser			
510	515	520	
tcc gaa gat tcc agt gaa gag gag aaa aaa aag aag ccc aaa gct act			1698
Ser Glu Asp Ser Ser Glu Glu Lys Lys Lys Lys Pro Lys Ala Thr			
525	530	535	
acc cct aaa ata cag gca agc aag gcc aat ggc act cca gct tct ctg			1746

Thr Pro Lys Ile Gln Ala Ser Lys Ala Asn Gly Thr Pro Ala Ser Leu		
540	545	550
aat gga aaa gca gcc aag gaa agt gag gag gaa gag gag gag gaa gaa		1794
Asn Gly Lys Ala Ala Lys Glu Ser Glu Glu Glu Glu Glu Glu Glu		
555	560	565
aca gaa gag aag aaa aag gca gct ggg acc aag cca ggt tca ggc aaa		1842
Thr Glu Glu Lys Lys Ala Ala Gly Thr Lys Pro Gly Ser Gly Lys		
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aaa cgg aag cag aat gag acc gca gat gaa gca aca act cct caa gct		1890
Lys Arg Lys Gln Asn Glu Thr Ala Asp Glu Ala Thr Thr Pro Gln Ala		
590	595	600
aag aaa gtt aag ctc gag acc ccc aat acg ttt cca aaa agg aag aag		1938
Lys Lys Val Lys Leu Glu Thr Pro Asn Thr Phe Pro Lys Arg Lys Lys		
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Gly Glu Arg Arg Ala Ser Ser Pro Phe Arg Arg Val Arg Glu Glu Glu		
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att gag gtg gac tct cga gtg gcg gac aat tcc ttt gat gcc aag cga		2034
Ile Glu Val Asp Ser Arg Val Ala Asp Asn Ser Phe Asp Ala Lys Arg		
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ggt gca gct gga gac tgg ggg gag cga gcc aat cag gtt ctg aag ttc		2082
Gly Ala Ala Gly Asp Trp Gly Glu Arg Ala Asn Gln Val Leu Lys Phe		
650	655	660
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acc aaa ggc aag tcc ttc cgg cat gaa aaa acg aag aag aag cga ggc		2130
Thr Lys Gly Lys Ser Phe Arg His Glu Lys Thr Lys Lys Arg Gly		
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agc tac cgg gga ggc tcc atc tct gtc cag gtc aat tcc gtc aaa ttc		2178
Ser Tyr Arg Gly Ser Ile Ser Val Gln Val Asn Ser Val Lys Phe		
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Asp Ser Glu		
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Leu Val Leu Arg Phe Leu Arg Asp Ser Gln Leu Ser Glu Val Ala Ser		
20	25	30

Lys Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser		
35	40	45

Ser Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Thr Lys Ala Pro		
50	55	60

Lys Val Lys Leu Gln Ser Asn Gly Pro Val Thr Lys Lys Ala Lys Lys			
65	70	75	80

Glu Thr Ser Ser Asp Ser Ser Glu Asp Ser Ser Glu Asp Glu Asp		
85	90	95

Lys Lys Ala Gln Gly Leu Pro Thr Gln Lys Ala Ala Ala Gln Val Lys

100

105

110

Arg Ala Ser Val Pro Gln His Ala Gly Lys Ala Ala Ala Lys Ala Ser
115 120 125

Glu Ser Ser Ser Glu Glu Ser Ser Glu Glu Glu Glu Asp Lys
130 135 140

Lys Lys Lys Pro Val Gln Lys Ala Ala Lys Pro Gln Ala Lys Ala Val
145 150 155 160

Arg Pro Pro Ala Lys Lys Ala Glu Ser Ser Glu Ser Asp Ser Asp Ser
165 170 175

Asp Ser Asp Ser Ser Ser Glu Glu Thr Pro Gln Thr Gln Lys Pro
180 185 190

Lys Ala Ala Val Ala Ala Lys Ala Gln Thr Lys Ala Glu Ala Lys Pro
195 200 205

Gly Thr Pro Ala Lys Ala Gln Pro Lys Val Ala Asn Gly Lys Ala Ala
210 215 220

Ala Ser Ser Ser Ser Ser Ser Asp Asp Ser Glu Glu Glu Lys
225 230 235 240

Lys Ala Ala Ala Pro Pro Lys Lys Thr Val Pro Lys Lys Gln Val Val
245 250 255

Ala Lys Ala Pro Val Lys Val Ala Ala Ala Pro Thr Gln Lys Ser Ser
260 265 270

Ser Ser Glu Asp Ser Ser Glu Glu Glu Glu Gly Gln Arg Gln Pro
275 280 285

Met Lys Lys Lys Ala Gly Pro Tyr Ser Ser Val Pro Pro Pro Ser Val
290 295 300

Pro Leu Pro Lys Lys Ser Pro Gly Thr Gln Ala Pro Lys Lys Ala Ala
305 310 315 320

Ala Gln Thr Gln Pro Ala Asp Ser Ser Asp Asp Ser Ser Asp Asp Ser
325 330 335

Asp Ser Ser Ser Glu Glu Lys Lys Pro Pro Ala Lys Thr Val Val

340

345

350

Ser Lys Thr Pro Ala Lys Ala Ala Pro Val Lys Lys Lys Ala Glu Ser
355 360 365

Ser Ser Asp Ser Ser Asp Ser Asp Ser Ser Glu Asp Glu Ala Pro Ala
370 375 380

Lys Pro Val Ser Thr Thr Lys Ser Pro Lys Pro Ala Val Thr Pro Lys
385 390 395 400

Pro Ser Ala Ala Lys Ala Val Thr Thr Pro Lys Gln Pro Ala Gly Ser
405 410 415

Asn Gln Lys Pro Gln Ser Arg Lys Ala Asp Ser Ser Ser Glu Glu
420 425 430

Glu Ser Ser Ser Glu Glu Glu Ala Ser Lys Lys Ser Ala Thr
435 440 445

Thr Pro Lys Ala Lys Val Thr Ala Lys Ala Ala Pro Ala Lys Gln Ala
450 455 460

Pro Gln Ala Ala Gly Asp Ser Ser Ser Asp Ser Asp Ser Ser Ser Ser
465 470 475 480

Glu Glu Glu Lys Thr Pro Lys Pro Pro Ala Lys Lys Lys Ala Ala
485 490 495

Gly Gly Ala Val Ser Thr Pro Ala Pro Gly Lys Lys Ala Glu Ala Lys
500 505 510

Ser Ser Ser Ser Ser Ser Ser Ser Glu Asp Ser Ser Glu Glu
515 520 525

Glu Lys Lys Lys Pro Lys Ala Thr Thr Pro Lys Ile Gln Ala Ser
530 535 540

Lys Ala Asn Gly Thr Pro Ala Ser Leu Asn Gly Lys Ala Ala Lys Glu
545 550 555 560

Ser Glu Glu Glu Glu Glu Glu Thr Glu Glu Lys Lys Lys Ala
565 570 575

Ala Gly Thr Lys Pro Gly Ser Gly Lys Lys Arg Lys Gln Asn Glu Thr

580

585

590

Ala Asp Glu Ala Thr Thr Pro Gln Ala Lys Lys Val Lys Leu Glu Thr
595 600 605

Pro Asn Thr Phe Pro Lys Arg Lys Lys Gly Glu Arg Arg Ala Ser Ser
610 615 620

Pro Phe Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val
625 630 635 640

Ala Asp Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly
645 650 655

Glu Arg Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg
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Ala Thr Pro Ala Glu Ala Ala Gln Ser Asp Arg His Ser Leu Leu Glu
15 20 25

cac agc cgc gag ttc ttg gac ttc tgg gac att gcg aaa ccg gat 147
His Ser Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Asp
30 35 40

cag gaa acg cgg ctc cgg gcc acg gag aag ttg ttg gag tac ttg cgc 195
Gln Glu Thr Arg Leu Arg Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg
45 50 55 60

aca agg ccc aat gat tcg gag atg aaa tat gcc ctg aag cgc cta atc 243
Thr Arg Pro Asn Asp Ser Glu Met Lys Tyr Ala. Leu Lys Arg Leu Ile

65

70

75

act ggg ctt ggg gtg ggc cga gaa gcc gct acg gcc tgc tac agc ctg Thr Gly Leu Gly Val Gly Arg Glu Ala Ala Thr Ala Cys Tyr Ser Leu 80	85	90	291
gcg ctg gca cag ctg ttg cag tct ttt gaa gac atc cca ttg tgt gac Ala Leu Ala Gln Leu Leu Gln Ser Phe Glu Asp Ile Pro Leu Cys Asp 95	100	105	339
atc ctg gat cag ata caa gaa aaa tac agc cta caa gcc atg aac aag Ile Leu Asp Gln Ile Gln Glu Lys Tyr Ser Leu Gln Ala Met Asn Lys 110	115	120	387
gca atg atg aga cct agt ctc ttt gca aac ctt ttt gga gtg cta gcc Ala Met Met Arg Pro Ser Leu Phe Ala Asn Leu Phe Gly Val Leu Ala 125	130	135	435
ctc ttt cag tca ggc cgc cta gtg aag gac aaa gag gcc ctg atg aag Leu Phe Gln Ser Gly Arg Leu Val Lys Asp Lys Glu Ala Leu Met Lys 145	150	155	483
tcc gtg caa ttg ctg aag atc ctg tcc caa cac ccc aac cac tta cag Ser Val Gln Leu Leu Lys Ile Leu Ser Gln His Pro Asn His Leu Gln 160	165	170	531
gga cag cca ata aag gct ctg gtg gac atc ctc tct gag gtc cca gag Gly Gln Pro Ile Lys Ala Leu Val Asp Ile Leu Ser Glu Val Pro Glu 175	180	185	579
tcc atg ttc cag gag atc ctg cca aag gtc ctc aag ggt aac atg aaa Ser Met Phe Gln Glu Ile Leu Pro Lys Val Leu Lys Gly Asn Met Lys 190	195	200	627
gtg atc ctc cgc tct ccc aag tac ttg gag ctc ttc ctc ctg gct aag Val Ile Leu Arg Ser Pro Lys Tyr Leu Glu Leu Phe Leu Ala Lys 205	210	215	675
cag agg gtg ccg aca aag ctc gag tca ctc atg ggc tcg gtt gac cta Gln Arg Val Pro Thr Lys Leu Glu Ser Leu Met Gly Ser Val Asp Leu 225	230	235	723
ttc tca gaa gac aat att ccc agt ctg gtg aac atc ctg aag gtg gcc Phe Ser Glu Asp Asn Ile Pro Ser Leu Val Asn Ile Leu Lys Val Ala 240	245	250	771
gcc aac tct gtc aag aag gag cac aag ctg cct aat gtg gct ctg gac Ala Asn Ser Val Lys Lys Glu His Lys Leu Pro Asn Val Ala Leu Asp 255	260	265	819
ctg ctc cgc ctg gct ctc aag gag agc aga ttc gaa ctg ttc tgg aag Leu Leu Arg Leu Ala Leu Lys Glu Ser Arg Phe Glu Leu Phe Trp Lys 270	275	280	867
aag gtt ttg gag gag ggg ctg ctg aag aat ccg tcc tgg aca tcc agc Lys Val Leu Glu Glu Gly Leu Leu Lys Asn Pro Ser Trp Thr Ser Ser 285	290	295	915
tac atg tgc ttc cgc cta ctg ggt gcg tct ctg ccg ctt ctg tca gag Tyr Met Cys Phe Arg Leu Leu Gly Ala Ser Leu Pro Leu Leu Ser Glu			963

305	310	315	
gag cag ttg cag ttg gtg atg cga gga gac ttg atc cgc cat ttt ggg Glu Gln Leu Gln Leu Val Met Arg Gly Asp Leu Ile Arg His Phe Gly 320	325	330	1011
gag aac atg gtt att tct aag ccc caa aac cta ttt aag atc atc cca Glu Asn Met Val Ile Ser Lys Pro Gln Asn Leu Phe Lys Ile Ile Pro 335	340	345	1059
gag ata agt aca tac gtg ggt acc ttc cta gag ggg tgc cag gat gac Glu Ile Ser Thr Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp 350	355	360	1107
cct aag cgg cag ttg act atg atg gtg gcc ttt aca acc atc acc aat Pro Lys Arg Gln Leu Thr Met Met Val Ala Phe Thr Thr Ile Thr Asn 365	370	375	1155
caa ggt ctc cct gtc atg cct acc ttc tgg cgt gtc acg cgg ttt ttg Gln Gly Leu Pro Val Met Pro Thr Phe Trp Arg Val Thr Arg Phe Leu 385	390	395	1203
aat gct gaa gcc ctg cag agc tat gtg gcc tgg tgg cgg gac atg ttc Asn Ala Glu Ala Leu Gln Ser Tyr Val Ala Trp Leu Arg Asp Met Phe 400	405	410	1251
ctg cag cct gac ctg aac tcc ttg gtt gac ttc agc act gcc aac cag Leu Gln Pro Asp Leu Asn Ser Leu Val Asp Phe Ser Thr Ala Asn Gln 415	420	425	1299
aag aga gct cag gac gcc tcg ttg aat gtg cct gag cga gct gta ttc Lys Arg Ala Gln Asp Ala Ser Leu Asn Val Pro Glu Arg Ala Val Phe 430	435	440	1347
cgg ctc cgg aag tgg atc atc cac cgc ctg gtc agc ctt gtg gat cat Arg Leu Arg Lys Trp Ile Ile His Arg Leu Val Ser Leu Val Asp His 445	450	455	1395
ttg cat ctg gag aag gat gaa gct gtg gtt gag caa ata gcc agg ttt Leu His Leu Glu Lys Asp Glu Ala Val Val Glu Gln Ile Ala Arg Phe 465	470	475	1443
tgc ttg ttc cat gcc ttc ttt aag acg aag aag gct acg ccc cag atc Cys Leu Phe His Ala Phe Phe Lys Thr Lys Lys Ala Thr Pro Gln Ile 480	485	490	1491
cca gag acg aag cag cac ttc tcc cct ttg gac gac cgc aac cgt Pro Glu Thr Lys Gln His Phe Ser Phe Pro Leu Asp Asp Arg Asn Arg 495	500	505	1539
ggg gtc ttt gtc agt gcc ttc agc cta ctg cag acg ctc agt gtg Gly Val Phe Val Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Val 510	515	520	1587
aag ttc agg cag aca cca gac ctg gct gaa aat ggg aag cct tgg act Lys Phe Arg Gln Thr Pro Asp Leu Ala Glu Asn Gly Lys Pro Trp Thr 525	530	535	1635
tac cgc ctg gtt cag ttg gca gac atg ctg ttg aac cat aac cgc aat Tyr Arg Leu Val Gln Leu Ala Asp Met Leu Leu Asn His Asn Arg Asn			1683

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gta acc agt gtg aca tcc ttg aca aca cag cag cgt cag gac Val Thr Ser Val Thr Ser Leu Thr Thr Gln Gln Arg Gln Ala Trp Asp 560	565	570	1731
cag atg atg agt act ctg aag gaa tta gag gcc cgcc tcc tct gag acc Gln Met Met Ser Thr Leu Lys Glu Leu Glu Ala Arg Ser Ser Glu Thr 575	580	585	1779
agg gcc att gcc ttc cag cac ctg ctg ctt ctg gtg ggc ctc cac atc Arg Ala Ile Ala Phe Gln His Leu Leu Leu Val Gly Leu His Ile 590	595	600	1827
ttc aag tcc cct gca gaa agc tgt gat gtc cta gga gac att cag act Phe Lys Ser Pro Ala Glu Ser Cys Asp Val Leu Gly Asp Ile Gln Thr 605	610	615	1875
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gcc aaa gcc tcc cag gag cca gta tgg gtg gag gtg atg gtg gag atc Ala Lys Ala Ser Gln Glu Pro Val Trp Val Glu Val Met Val Glu Ile 640	645	650	1971
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gga gag gac gaa gac tca gat aat gag gac aat aag aac tca gag agt Gly Glu Asp Glu Asp Ser Asp Asn Glu Asp Asn Lys Asn Ser Glu Ser 720	725	730	2211
gac atg gac agt gag gat ggg gaa gaa agt gaa gag gag gac cgt gac Asp Met Asp Ser Glu Asp Gly Glu Glu Ser Glu Glu Glu Asp Arg Asp 735	740	745	2259
aaa gat gtg gac cca ggc ttc cgt caa cag ttg atg gaa gtg tta aaa Lys Asp Val Asp Pro Gly Phe Arg Gln Gln Leu Met Glu Val Leu Lys 750	755	760	2307
gct ggg aat gca ttg ggt gga gtg gac aac gag gag gag gag ctt Ala Gly Asn Ala Leu Gly Gly Val Asp Asn Glu Glu Glu Glu Glu Leu 765	770	775	2355
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cgc atc ttc atg cac cac ctg tgt cgt gcc cgc cgc tac tgc cac gag Arg Ile Phe Met His His Leu Cys Arg Ala Arg Arg Tyr Cys His Glu 880	885	890	2691
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aat gcc tct ctg tac ctg ctg cga gtc ctc aag ggc aac acc aat aag Asn Ala Ser Leu Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Asn Lys 925	930	935	2835
agg cac caa gat ggt cat aag tta cac gga gct gac aca gag gac tca Arg His Gln Asp Gly His Lys Leu His Gly Ala Asp Thr Glu Asp Ser 945	950	955	2883
gag gac cag gct aac tgc tta gac ttg gac ttt gtg acc cgg gtg Glu Asp Gln Ala Ala Asn Cys Leu Asp Leu Asp Phe Val Thr Arg Val 960	965	970	2931
tat tca gca tca ctg gaa tct ctt ctg acc aag cgt aac agc tca ctt Tyr Ser Ala Ser Leu Glu Ser Leu Leu Thr Lys Arg Asn Ser Ser Leu 975	980	985	2979
acg gtc ccc atg ttc ctc agc ctc ttc tcc aga tac cca gtg atc tgt Thr Val Pro Met Phe Leu Ser Leu Phe Ser Arg Tyr Pro Val Ile Cys 990	995	1000	3027
aag aac ctg ctt ccc gtc ctg gct cag cat gtg gct ggc cca tct Lys Asn Leu Leu Pro Val Leu Ala Gln His Val Ala Gly Pro Ser 1005	1010	1015	3072
cgg ccc cgc cat cag gcc cag gca tgc ctg atg ctc cag aag act Arg Pro Arg His Gln Ala Gln Ala Cys Leu Met Leu Gln Lys Thr			3117

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Leu Ser Ala Arg Glu Leu	Arg Val Cys Phe Glu	Asp Pro Glu Trp	
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Glu Gln Leu Ile Thr Gln	Leu Leu Gly Lys Ala	Thr Gln Thr Leu	
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Gln Thr Leu Gly Glu Ala	Gln Ser Lys Gly Glu	His Gln Lys Glu	
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Leu Ser Ile Leu Glu Leu	Leu Asn Thr Leu Leu	Arg Thr Val Asn	
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His Glu Lys Leu Ser Val	Asp Leu Thr Ala Pro	Leu Gly Val Leu	
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Gln Ser Lys Gln Gln Lys	Leu Gln Gln Ser Leu	Gln Gln Gly Asn	
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His Ser Ser Gly Ser Asn	Arg Leu Tyr Asp Leu	Tyr Trp Gln Ala	
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Met Arg Met Leu Gly Val	Gln Arg Pro Lys Ser	Glu Lys Lys Asn	
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Arg Lys Lys Lys Gly Phe	Leu Pro Glu Thr Lys	Lys Arg Lys Lys	
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Leu Lys Ser Glu Gly Thr	Thr Pro Glu Lys Asn	Ala Ala Ser Gln	
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Gln Asp Ala Val Thr Glu	Gly Ala Met Pro Ala	Ala Thr Gly Lys	
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Asp Gln Pro Pro Ser Thr	Gly Lys Lys Lys Arg	Lys Arg Val Lys	
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Ala Ser Thr Pro Ser Gln	Val Asn Gly Ile Thr	Gly Ala Lys Ser	
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Pro Ala Pro Ser Asn Pro	Thr Leu Ser Pro Ser	Thr Pro Ala Lys	

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Thr Pro Lys Leu Gln Lys	Lys Lys Glu Lys Leu	Ser Gln Val Asn	
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Gly Ala Thr Pro Val Ser	Pro Ile Glu Pro Glu	Ser Lys Lys His	
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His Gln Glu Ala Leu Ser	Thr Lys Glu Val Ile	Arg Lys Ser Pro	
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His Pro Gln Ser Ala Leu	Pro Lys Lys Arg Ala	Arg Leu Ser Leu	
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Asp Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly Leu Gly			
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Val Gly Arg Glu Ala Ala Thr Ala Cys Tyr Ser Leu Ala Leu Ala Gln			
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Leu Leu Gln Ser Phe Glu Asp Ile Pro Leu Cys Asp Ile Leu Asp Gln
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Ile Gln Glu Lys Tyr Ser Leu Gln Ala Met Asn Lys Ala Met Met Arg
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Pro Ser Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe Gln Ser
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Gly Arg Leu Val Lys Asp Lys Glu Ala Leu Met Lys Ser Val Gln Leu
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Leu Lys Ile Leu Ser Gln His Pro Asn His Leu Gln Gly Gln Pro Ile
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Lys Ala Leu Val Asp Ile Leu Ser Glu Val Pro Glu Ser Met Phe Gln
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Glu Ile Leu Pro Lys Val Leu Lys Gly Asn Met Lys Val Ile Leu Arg
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Ser Pro Lys Tyr Leu Glu Leu Phe Leu Leu Ala Lys Gln Arg Val Pro
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Thr Lys Leu Glu Ser Leu Met Gly Ser Val Asp Leu Phe Ser Glu Asp
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Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Lys Arg Gln
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Asp Ala Ser Leu Asn Val Pro Glu Arg Ala Val Phe Arg Leu Arg Lys
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Lys Asp Glu Ala Val Val Glu Gln Ile Ala Arg Phe Cys Leu Phe His
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Gln His Phe Ser Phe Pro Leu Asp Asp Arg Asn Arg Gly Val Phe Val
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Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Val Lys Phe Arg Gln
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Thr Pro Asp Leu Ala Glu Asn Gly Lys Pro Trp Thr Tyr Arg Leu Val
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545 550 555 560

Thr Ser Leu Thr Thr Gln Gln Arg Gln Ala Trp Asp Gln Met Met Ser
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Thr Leu Lys Glu Leu Glu Ala Arg Ser Ser Glu Thr Arg Ala Ile Ala
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Phe Gln His Leu Leu Leu Val Gly Leu His Ile Phe Lys Ser Pro
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Ala Glu Ser Cys Asp Val Leu Gly Asp Ile Gln Thr Cys Ile Lys Lys
610 615 620

Ser Met Glu Gln Asn Pro Arg Arg Ser Arg Ser Arg Ala Lys Ala Ser
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Leu Ala Gln Pro Ser Asn Leu Met Arg Gln Val Val Arg Ser Val Phe
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Gly His Ile Cys Pro His Leu Thr Pro Arg Cys Leu Gln Leu Ile Leu
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Ala Val Leu Ser Pro Val Thr Asn Glu Asp Glu Asp Asp Asn Val Val
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Asp Ser Asp Asn Glu Asp Asn Lys Asn Ser Glu Ser Asp Met Asp Ser
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Lys Lys Leu Arg Arg Asp Phe Gln Ile Arg Ala Leu Asp Leu Ile Glu
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His His Leu Cys Arg Ala Arg Arg Tyr Cys His Glu Val Gly Pro Cys
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Ser Gln Ala Asp Ala Ser Val Ala Leu Tyr Tyr Phe Asn Ala Ser Leu
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Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Asn Lys Arg His Gln Asp
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Gly His Lys Leu His Gly Ala Asp Thr Glu Asp Ser Glu Asp Gln Ala
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Ala Asn Cys Leu Asp Leu Asp Phe Val Thr Arg Val Tyr Ser Ala Ser
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Leu Glu Ser Leu Leu Thr Lys Arg Asn Ser Ser Leu Thr Val Pro Met
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Phe Leu Ser Leu Phe Ser Arg Tyr Pro Val Ile Cys Lys Asn Leu Leu
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Glu Leu Arg Val Cys Phe Glu Asp Pro Glu Trp Glu Gln Leu Ile
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Glu Ala Gln Ser Lys Gly Glu His Gln Lys Glu Leu Ser Ile Leu
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Glu Leu Leu Asn Thr Leu Leu Arg Thr Val Asn His Glu Lys Leu
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Ser Val Asp Leu Thr Ala Pro Leu Gly Val Leu Gln Ser Lys Gln
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Gln Lys Leu Gln Gln Ser Leu Gln Gln Gly Asn His Ser Ser Gly
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Met Gly Arg Arg Ala Arg Gly Arg Arg Phe Gln Gln
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Pro Pro Gln Pro Glu Gly Glu Asp Ala Ser Asp Gly Gly Arg Lys
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Arg Gly Gln Ala Gly Trp Glu Gly Gly Tyr Pro Glu Ile Val Lys Glu
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Asn Lys Leu Phe Glu His Tyr Tyr Gln Glu Leu Lys Ile Val Pro Glu
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Gly Glu Trp Asp Gln Phe Met Glu Ser Leu Arg Glu Pro Leu Pro Ala
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Cys	Leu	Lys	Asn	Lys	Tyr	Phe	Lys	Glu	Leu	Glu	Asp	Leu	Glu	Val	Asp		
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Gly	Gln	Lys	Val	Glu	Val	Pro	Gln	Pro	Leu	Ser	Trp	Tyr	Pro	Glu	Glu		
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ctt	gcc	tgg	cat	aca	aac	tta	agt	cgg	aaa	atc	ttg	agg	aag	tcc	ccg	495	
Leu	Ala	Trp	His	Thr	Asn	Leu	Ser	Arg	Lys	Ile	Leu	Arg	Lys	Ser	Pro		
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ttg	ttg	gca	aag	ttc	cat	cag	ttc	ctg	gtc	agc	gag	act	gag	tct	gga	543	
Leu	Leu	Ala	Lys	Phe	His	Gln	Phe	Leu	Val	Ser	Glu	Thr	Glu	Ser	Gly		
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aac	atc	agc	cgc	cag	gag	gct	gtc	agc	atg	atc	ccc	cca	ctg	ctg	ctc	591	
Asn	Ile	Ser	Arg	Gln	Glu	Ala	Val	Ser	Met	Ile	Pro	Pro	Leu	Leu	Leu		
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aac	gtg	gag	cca	cac	cat	aag	atc	tta	gac	atg	tgt	gca	gcc	cct	gga	639	
Asn	Val	Glu	Pro	His	His	Lys	Ile	Leu	Asp	Met	Cys	Ala	Ala	Pro	Gly		
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tcc	aag	acc	aca	cag	tta	att	gaa	atg	ttg	cat	gca	gac	atg	agt	gtg	687	
Ser	Lys	Thr	Thr	Gln	Leu	Ile	Glu	Met	Leu	His	Ala	Asp	Met	Ser	Val		
190							195					200					
ccc	ttt	cca	gag	gga	ttt	gta	atc	gca	aat	gac	gtg	gac	aac	aag	cgc	735	
Pro	Phe	Pro	Glu	Gly	Phe	Val	Ile	Ala	Asn	Asp	Val	Asp	Asn	Lys	Arg		
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Val	Pro	Cys	Ser	Gly	Asp	Gly	Thr	Met	Arg	Lys	Asn	Ile	Asp	Val	Trp		
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Lys	Lys	Trp	Thr	Leu	Asn	Ser	Leu	Gln	Leu	His	Gly	Leu	Gln	Leu			
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Val	Tyr	Ser	Thr	Cys	Ser	Leu	Asn	Pro	Val	Glu	Asp	Glu	Ala	Val	Ile		
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Ser Ala Glu Leu Pro Gly Leu Lys Trp Met Pro Gly Val Ser Gln Trp			
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Lys Val Met Thr Arg Asp Gly Gln Trp Phe Ala Asp Trp His Glu Val			
365	370	375	380
ccc cag ggc agg cat aca caa atc cga cct acc atg ttc cca cca acg			1263
Pro Gln Gly Arg His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Thr			
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Asp Leu Glu Lys Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile			
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Leu Pro His His Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val			
415	420	425	
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Lys Lys Ala Pro Met Pro Trp Asn Lys Arg Gln Pro Lys Val Gln Asn			
430	435	440	
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Lys Ser Ala Glu Ala Arg Glu Pro Arg Val Ser Ser His Val Ala Ala			
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aca gag gga aat ccc agt gac cag tct gag ctg gaa agt cag atg ata			1503
Thr Glu Gly Asn Pro Ser Asp Gln Ser Glu Leu Glu Ser Gln Met Ile			
465	470	475	
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Thr Gly Ala Gly Asp Leu Glu Thr Ala His Asn Thr Glu Asn Thr Glu			
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Ser Asn Glu Lys Lys Asp Gly Val Cys Gly Pro Pro Ser Lys Lys			
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atg aag ttg ttt gga ttt aaa gaa gat cca ttt gta ttc att cct gaa			1647
Met Lys Leu Phe Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro Glu			
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Asp Asp Pro Leu Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp Pro			
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tca ttc ccg agg atg aat ctg tta acc cga acc aca gaa gga aag aag			1743
Ser Phe Pro Arg Met Asn Leu Leu Thr Arg Thr Glu Gly Lys Lys			
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cgg cag ctt tat atg gtc tcc aag gag ctg agg aat gta ctg ctg aac			1791
Arg Gln Leu Tyr Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu Asn			
560	565	570	
aac agc gag aag atg aag gtc att aac act ggg ata aaa gtc tgg tgt			1839

Asn Ser Glu Lys Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp Cys			
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Arg Asn Asn Ser Gly Glu Phe Asp Cys Ala Phe Arg Leu Ala Gln			
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Glu Gly Ile Tyr Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile Thr			
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gta tca atg gaa gac gtg aag aca ctg ttg acc cag gag aac cca ttc			1983
Val Ser Met Glu Asp Val Lys Thr Leu Thr Gln Glu Asn Pro Phe			
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Phe Arg Lys Leu Ser Ser Glu Ala Tyr Ser Gln Val Lys Asp Leu Ala			
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Lys Gly Ser Val Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro Asp			
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Ile Arg Thr Phe Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg Met			
685	690	695	700
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Lys Gln Thr Ala Gln Asp Pro Cys Val Pro Asp Ser Val Pro Gly Cys			
735	740	745	
gat gca gct gca gct gag cca tcc cg ^g tga aggagtcttc acacaatgaa			2369
Asp Ala Ala Ala Glu Pro Ser Arg			
750	755		
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gagtggtggc cacagtctgt taggagtcgc tttgcagag tggatacatg tttctgctgt			2489
taaaggctaa cagccttgc agaagttcag atcccttgtt ggccagtatt gacctagttc			2549
tctaaaacga cagtaaaagt ctacaagtct ttggaaagca gctctatcta tctatgctt			2609
aataactttct ggactgcaca ccagtgtgct gtgcagtcat gctgacactg aggtctcagg			2669
tgacttctgt gcctttgtga taaagggtga gataagccat ctcagaggga aggctggta			2729
atcatgacag cagtttggg gacccttgt gcttatcctg gagttgttt aagtggggtg			2789

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aa 2851

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Gly Trp Glu Gly Gly Tyr Pro Glu Ile Val Lys Glu Asn Lys Leu Phe
35 40 45

Glu His Tyr Tyr Gln Glu Leu Lys Ile Val Pro Glu Gly Glu Trp Asp
50 55 60

Gln Phe Met Glu Ser Leu Arg Glu Pro Leu Pro Ala Thr Leu Arg Ile
65 70 75 80

Thr Gly Tyr Lys Ser His Ala Lys Glu Ile Leu His Cys Leu Lys Asn
85 90 95

Lys Tyr Phe Lys Glu Leu Glu Asp Leu Glu Val Asp Gly Gln Lys Val
100 105 110

Glu Val Pro Gln Pro Leu Ser Trp Tyr Pro Glu Glu Leu Ala Trp His
115 120 125

Thr Asn Leu Ser Arg Lys Ile Leu Arg Lys Ser Pro Leu Leu Ala Lys
130 135 140

Phe His Gln Phe Leu Val Ser Glu Thr Glu Ser Gly Asn Ile Ser Arg
145 150 155 160

Gln Glu Ala Val Ser Met Ile Pro Pro Leu Leu Leu Asn Val Glu Pro
165 170 175

His His Lys Ile Leu Asp Met Cys Ala Ala Pro Gly Ser Lys Thr Thr
180 185 190

Gln Leu Ile Glu Met Leu His Ala Asp Met Ser Val Pro Phe Pro Glu
195 200 205

Gly Phe Val Ile Ala Asn Asp Val Asp Asn Lys Arg Cys Tyr Leu Leu
210 215 220

Val His Gln Ala Lys Arg Leu Ser Ser Pro Cys Ile Met Val Val Asn
225 230 235 240

His Asp Ala Ser Ser Ile Pro Arg Leu Thr Val Asp Val Asp Gly Arg
245 250 255

Lys Glu Ile Leu Phe Tyr Asp Arg Ile Leu Cys Asp Val Pro Cys Ser
260 265 270

Gly Asp Gly Thr Met Arg Lys Asn Ile Asp Val Trp Lys Lys Trp Thr
275 280 285

Thr Leu Asn Ser Leu Gln Leu His Gly Leu Gln Leu Arg Ile Ala Thr
290 295 300

Arg Gly Ala Glu Gln Leu Ala Glu Gly Gly Arg Met Val Tyr Ser Thr
305 310 315 320

Cys Ser Leu Asn Pro Val Glu Asp Glu Ala Val Ile Ala Ala Leu Leu
325 330 335

Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val Ser Ala Glu Leu
340 345 350

Pro Gly Leu Lys Trp Met Pro Gly Val Ser Gln Trp Lys Val Met Thr
355 360 365

Arg Asp Gly Gln Trp Phe Ala Asp Trp His Glu Val Pro Gln Gly Arg
370 375 380

His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Thr Asp Leu Glu Lys
385 390 395 400

Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile Leu Pro His His
405 410 415

Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val Lys Lys Ala Pro
420 425 430

Met Pro Trp Asn Lys Arg Gln Pro Lys Val Gln Asn Lys Ser Ala Glu
435 440 445

Ala Arg Glu Pro Arg Val Ser Ser His Val Ala Ala Thr Glu Gly Asn
450 455 460

Pro Ser Asp Gln Ser Glu Leu Glu Ser Gln Met Ile Thr Gly Ala Gly
465 470 475 480

Asp Leu Glu Thr Ala His Asn Thr Glu Asn Thr Glu Ser Asn Glu Lys
485 490 495

Lys Asp Gly Val Cys Gly Pro Pro Pro Ser Lys Lys Met Lys Leu Phe
500 505 510

Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro Glu Asp Asp Pro Leu
515 520 525

Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp Pro Ser Phe Pro Arg
530 535 540

Met Asn Leu Leu Thr Arg Thr Thr Glu Gly Lys Lys Arg Gln Leu Tyr
545 550 555 560

Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu Asn Asn Ser Glu Lys
565 570 575

Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp Cys Arg Asn Asn Ser
580 585 590

Gly Glu Glu Phe Asp Cys Ala Phe Arg Leu Ala Gln Glu Gly Ile Tyr
595 600 605

Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile Thr Val Ser Met Glu
610 615 620

Asp Val Lys Thr Leu Leu Thr Gln Glu Asn Pro Phe Phe Arg Lys Leu
625 630 635 640

Ser Ser Glu Ala Tyr Ser Gln Val Lys Asp Leu Ala Lys Gly Ser Val
645 650 655

Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro Asp Thr Leu Gln Cys
660 665 670

Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala Ser Ile Arg Thr Phe
675 680 685

Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg Met Met Gly Leu Glu
690 695 700

Val Leu Gly Glu Lys Lys Glu Gly Val Ile Leu Thr Asn Glu Asn
705 710 715 720

Ala Ala Ser Pro Glu Gln Pro Gly Asp Glu Asp Ala Lys Gln Thr Ala
725 730 735

Gln Asp Pro Cys Val Pro Asp Ser Val Pro Gly Cys Asp Ala Ala Ala
740 745 750

Ala Glu Pro Ser Arg
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1 5 10

ttg tca tgg acg gga ccc ctt cag gga cag cag cac cac ctt gtg gag 97
Leu Ser Trp Thr Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu
15 20 25

tac atg gaa cgc cga cta gct gcc tta gag gaa cgg ctg gcc caa tgc 145
Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys
30 35 40

cag gat cag agt agt cgg cat gct gcc gag ctt cgg gac ttc aaa aac 193
Gln Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
45 50 55 60

aag atg ttg cct ctc ctg gag gtg gca gag aag gag cgg gag acc ctc 241
Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Thr Leu
65 70 75

aga act gaa gca gac tcc atc tca gga aga gtg gac cgt ctt gaa agg 289
Arg Thr Glu Ala Asp Ser Ile Ser Gly Arg Val Asp Arg Leu Glu Arg
80 85 90

gag gta gac tat ctg gag aca cag aac cca gct ttg ccc tgt gta gag Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu	337
95 100 105	
ctg gat gag aag gtg act gga ggt cct gga gcc aaa ggc aag ggc cga Leu Asp Glu Lys Val Thr Gly Gly Pro Gly Ala Lys Gly Lys Gly Arg	385
110 115 120	
aga aat gag aaa tac gat atg gtg acg gac tgt agc tac aca gtc gct Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys Ser Tyr Thr Val Ala	433
125 130 135 140	
cag gtg agg tca atg aag atc ctg aag cgg ttt ggt ggt tca gct ggc Gln Val Arg Ser Met Lys Ile Leu Lys Arg Phe Gly Gly Ser Ala Gly	481
145 150 155	
cta tgg acc aag gat ccg ctg ggg cca gca gag aag atc tac gtg tta Leu Trp Thr Lys Asp Pro Leu Gly Pro Ala Glu Lys Ile Tyr Val Leu	529
160 165 170	
gac ggc acc cag aac gac acg gct ttt gtc ttc cca agg ctg cgt gac Asp Gly Thr Gln Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp	577
175 180 185	
tcc acc ctt gcc atg gct gcc cgg aaa gct tcc cga att cgg gtg ccc Phe Thr Leu Ala Met Ala Ala Arg Lys Ala Ser Arg Ile Arg Val Pro	625
190 195 200	
tcc ccc tgg gta ggc acg ggg cag ctg gtg tac ggt ggc ttc ctt tat Phe Pro Trp Val Gly Thr Gly Gln Leu Val Tyr Gly Phe Leu Tyr	673
205 210 215 220	
tat gct cga agg cct cct gga gga cct gga ggg ggt ggt gaa ttg gag Tyr Ala Arg Arg Pro Pro Gly Gly Pro Gly Gly Gly Glu Leu Glu	721
225 230 235	
aac act ctg cag ctg atc aaa ttt cac ttg gca aac cga aca gtg gtg Asn Thr Leu Gln Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val	769
240 245 250	
gat agc tca gtg ttc cct gca gag agc ctg ata ccc ccc tac ggc ctg Asp Ser Ser Val Phe Pro Ala Glu Ser Leu Ile Pro Pro Tyr Gly Leu	817
255 260 265	
aca gca gat aca tat atc gac ctg gca gct gat gag gag ggc ctg tgg Thr Ala Asp Thr Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp	865
270 275 280	
gct gtc tat gcc act cga gat gat gac agg cat ttg tgt cta gcc aag Ala Val Tyr Ala Thr Arg Asp Asp Asp Arg His Leu Cys Leu Ala Lys	913
285 290 295 300	
tta gac cca cag aca ctt gac aca gag cag cag tgg gac aca cca tgt Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys	961
305 310 315	
ccc aga gag aac gca gag gct ttt gtc atc tgt ggg acc ctg tac Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr	1009
320 325 330	

gtt gtc tat aac acc cgc cct gcc agt agg gct cgt att cag tgt tcc Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser	335 340 345	1057
ttc gat gcc agt ggt act ctc gcc cct gaa agg gca gca ctc tcc tat Phe Asp Ala Ser Gly Thr Leu Ala Pro Glu Arg Ala Ala Leu Ser Tyr	350 355 360	1105
ttt cca cgc cga tat ggt gcc cat gcc agc ctt cgc tat aac ccc cgt Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg	365 370 375 380	1153
gag cgc cag ctg tat gcc tgg gat gat ggc tat cag att gtc tac aaa Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys	385 390 395	1201
ttg gag atg aag aag gag gag gaa gtt taa gcagctagcc ttgtgcttt Leu Glu Met Lys Lys Glu Glu Val	400 405	1254
gattcttatg cccagacatt tatattcctg tgagctctcc tgcatcgat cttcaaaaac gaaggccagt ggtggtagct catataccct aatttctaaa ggacaaccaa attctcaagc		1314
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ctgtcctttg gagagggtca accccagaca gcaggcgaca gcattctgc cctcagtgatg accgaaggga gagaactcag agacaaagct gccctccctc cttccccct ccagtgttagg		1434
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Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser	
35 40 45	

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro	
50 55 60	

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Thr Leu Arg Thr Glu Ala
65 70 75 80

Asp Ser Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Leu Asp Glu Lys
100 105 110

Val Thr Gly Gly Pro Gly Ala Lys Gly Lys Gly Arg Arg Asn Glu Lys
115 120 125

Tyr Asp Met Val Thr Asp Cys Ser Tyr Thr Val Ala Gln Val Arg Ser
130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Ser Ala Gly Leu Trp Thr Lys
145 150 155 160

Asp Pro Leu Gly Pro Ala Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
165 170 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
180 185 190

Met Ala Ala Arg Lys Ala Ser Arg Ile Arg Val Pro Phe Pro Trp Val
195 200 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Tyr Ala Arg Arg
210 215 220

Pro Pro Gly Gly Pro Gly Gly Glu Leu Glu Asn Thr Leu Gln
225 230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
245 250 255

Phe Pro Ala Glu Ser Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
260 265 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
275 280 285

Thr Arg Asp Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
290 295 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
305 310 315 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
325 330 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
340 345 350

Gly Thr Leu Ala Pro Glu Arg Ala Ala Leu Ser Tyr Phe Pro Arg Arg
355 360 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
370 375 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Lys
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Lys Lys Glu Glu Val
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<220>
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<222> (48)..(1193)

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Arg Ala Ala Leu Thr Gly Phe Ala Val Leu Met Leu Leu Gln Ser Cys
5 10 15

tct gcg tac aag ctg gtc tgc tac ttc acc agc tgg tcc cag tac cgg 152
Ser Ala Tyr Lys Leu Val Cys Tyr Phe Thr Ser Trp Ser Gln Tyr Arg
20 25 30 35

gaa ggc gtt gga agc ttc tta cca gac gcc atc caa cct ttc ctg tgc 200
Glu Gly Val Gly Ser Phe Leu Pro Asp Ala Ile Gln Pro Phe Leu Cys
40 45 50

acc cac atc atc tac agc ttt gcc aac atc agc agc gac aac atg ctt 248
Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Ser Asp Asn Met Leu
55 60 65

agc aca tgg gag tgg aat gac gag tcg aac tat gac aag ctg aat aaa 296

Ser	Thr	Trp	Glu	Trp	Asn	Asp	Glu	Ser	Asn	Tyr	Asp	Lys	Leu	Asn	Lys	
70					75						80					
ctg	aag	acc	aga	aac	acc	aac	ctg	aag	acc	ctc	ctg	tct	gtt	gga	ggg	344
Leu	Lys	Thr	Arg	Asn	Thr	Asn	Leu	Lys	Thr	Leu	Leu	Ser	Val	Gly	Gly	
85					90						95					
tgg	aaa	ttt	ggc	gaa	aaa	aga	ttt	tcc	gag	att	gcc	tcc	aac	act	gag	392
Trp	Lys	Phe	Gly	Glu	Lys	Arg	Phe	Ser	Glu	Ile	Ala	Ser	Asn	Thr	Glu	
100					105					110				115		
aga	cgc	act	gtc	ttc	gtc	cg	tcg	gta	gcc	ccg	tcc	ctg	cgt	tct	tat	440
Arg	Arg	Thr	Ala	Phe	Val	Arg	Ser	Val	Ala	Pro	Phe	Leu	Arg	Ser	Tyr	
120					125					130						
ggc	ttt	gat	ggg	ctg	gat	ctc	gcc	tgg	ctc	tac	cct	cgc	tta	aga	gac	488
Gly	Phe	Asp	Gly	Leu	Asp	Leu	Ala	Trp	Leu	Tyr	Pro	Arg	Leu	Arg	Asp	
135				140						145						
aag	cag	tat	ttc	tcc	acc	ctg	atc	aag	gaa	ctg	aat	gcg	gaa	ttc	aca	536
Lys	Gln	Tyr	Phe	Ser	Thr	Leu	Ile	Lys	Glu	Leu	Asn	Ala	Glu	Phe	Thr	
150				155					160							
aag	gag	gtc	cag	cca	ggc	aga	gag	aaa	ctc	ctg	ctc	agc	gca	gct	ttg	584
Lys	Glu	Val	Gln	Pro	Gly	Arg	Glu	Lys	Leu	Leu	Leu	Ser	Ala	Ala	Leu	
165				170					175							
tca	gca	gga	aag	gtg	gcc	att	gac	act	ggc	tat	gac	atc	gcc	cag	ata	632
Ser	Ala	Gly	Lys	Val	Ala	Ile	Asp	Thr	Gly	Tyr	Asp	Ile	Ala	Gln	Ile	
180				185					190				195			
gcc	caa	cac	ctg	gat	ttt	atc	aat	ctc	atg	acc	tac	gat	ttc	cat	gga	680
Ala	Gln	His	Leu	Asp	Phe	Ile	Asn	Leu	Met	Thr	Tyr	Asp	Phe	His	Gly	
200				205					210							
gtc	tgg	cgc	caa	atc	aca	ggc	cat	cac	agc	ccc	ctc	ttc	caa	ggc	cag	728
Val	Trp	Arg	Gln	Ile	Thr	Gly	His	His	Ser	Pro	Leu	Phe	Gln	Gly	Gln	
215				220					225							
aag	gac	act	agg	ttt	gac	aga	tac	agc	aat	gtg	aac	tat	gcc	gtg	cag	776
Lys	Asp	Thr	Arg	Phe	Asp	Arg	Tyr	Ser	Asn	Val	Asn	Tyr	Ala	Val	Gln	
230				235					240							
tac	atg	ata	cgt	ctg	gga	gcc	cag	gcc	agc	aag	cta	ctg	atg	ggc	atc	824
Tyr	Met	Ile	Arg	Leu	Gly	Ala	Gln	Ala	Ser	Lys	Leu	Leu	Met	Gly	Ile	
245				250					255							
ccc	acc	ttt	ggg	aag	agc	ttc	act	ctg	gca	tct	tct	gaa	aat	cag	ttg	872
Pro	Thr	Phe	Gly	Lys	Ser	Phe	Thr	Leu	Ala	Ser	Ser	Glu	Asn	Gln	Leu	
260				265					270			275				
gga	gct	cca	atc	tca	ggg	gaa	gga	tta	cca	ggc	cg	ttc	acc	aag	gag	920
Gly	Ala	Pro	Ile	Ser	Gly	Glu	Gly	Leu	Pro	Gly	Arg	Phe	Thr	Lys	Glu	
280				285					290							
gca	ggg	acc	ctg	gcc	tac	tac	gag	ata	tgc	gac	ttc	ctc	aaa	gga	gct	968
Ala	Gly	Thr	Leu	Ala	Tyr	Tyr	Glu	Ile	Cys	Asp	Phe	Leu	Lys	Gly	Ala	
295				300					305							
gaa	gta	cat	cga	ctc	tcc	aac	gag	aag	gtt	ccc	ttc	gct	acc	aag	ggc	1016

Glu Val His Arg Leu Ser Asn Glu Lys Val Pro Phe Ala Thr Lys Gly				
310	315	320		
aac cag tgg gtg ggg tat gag gac aag gag agt gtc aaa aac aag gtt				1064
Asn Gln Trp Val Gly Tyr Glu Asp Lys Glu Ser Val Lys Asn Lys Val				
325	330	335		
ggg ttc ctg aag gag aag aag ctg gca gga gcc atg gtg tgg gca ctg				1112
Gly Phe Leu Lys Glu Lys Leu Ala Gly Ala Met Val Trp Ala Leu				
340	345	350	355	
gat ttg gat gat ttc cag ggc acc tgt cag ccg aag gaa ttc ttc ccg				1160
Asp Leu Asp Asp Phe Gln Gly Thr Cys Gln Pro Lys Glu Phe Phe Pro				
360	365	370		
ctc acc aac gcc atc aag gat gcc ctg gct tag ctccccc tt cccatatggt				1213
Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala				
375	380			
accccccactc tctggccagg agtttaatct cttgcaatgt taagtcccc aactgagcct				1273
cagtttctcc ttcccttggc acctgtgtaa ggggccacag caggctcagc tatggagaac				1333
agggaaactag ggttaggacga tgggtggggtt gtgagagtca cagtgtgagc agatacacaa				1393
ccctgttaag gaatgcaa at tctcagactc taacctccct ttacccagcc tgaccAAagg				1453
acaccacttg gatcaagtag gcaaataatct tacaggattg agggaccata ctaattatac				1513
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Gln Ser Cys Ser Ala Tyr Lys Leu Val Cys Tyr Phe Thr Ser Trp Ser				
20	25	30		
Gln Tyr Arg Glu Gly Val Gly Ser Phe Leu Pro Asp Ala Ile Gln Pro				
35	40	45		
Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Ser Asp				
50	55	60		
Asn Met Leu Ser Thr Trp Glu Trp Asn Asp Glu Ser Asn Tyr Asp Lys				
65	70	75	80	

Leu Asn Lys Leu Lys Thr Arg Asn Thr Asn Leu Lys Thr Leu Leu Ser
85 90 95

Val Gly Gly Trp Lys Phe Gly Glu Lys Arg Phe Ser Glu Ile Ala Ser
100 105 110

Asn Thr Glu Arg Arg Thr Ala Phe Val Arg Ser Val Ala Pro Phe Leu
115 120 125

Arg Ser Tyr Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Arg
130 135 140

Leu Arg Asp Lys Gln Tyr Phe Ser Thr Leu Ile Lys Glu Leu Asn Ala
145 150 155 160

Glu Phe Thr Lys Glu Val Gln Pro Gly Arg Glu Lys Leu Leu Leu Ser
165 170 175

Ala Ala Leu Ser Ala Gly Lys Val Ala Ile Asp Thr Gly Tyr Asp Ile
180 185 190

Ala Gln Ile Ala Gln His Leu Asp Phe Ile Asn Leu Met Thr Tyr Asp
195 200 205

Phe His Gly Val Trp Arg Gln Ile Thr Gly His His Ser Pro Leu Phe
210 215 220

Gln Gly Gln Lys Asp Thr Arg Phe Asp Arg Tyr Ser Asn Val Asn Tyr
225 230 235 240

Ala Val Gln Tyr Met Ile Arg Leu Gly Ala Gln Ala Ser Lys Leu Leu
245 250 255

Met Gly Ile Pro Thr Phe Gly Lys Ser Phe Thr Leu Ala Ser Ser Glu
260 265 270

Asn Gln Leu Gly Ala Pro Ile Ser Gly Glu Gly Leu Pro Gly Arg Phe
275 280 285

Thr Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu
290 295 300

Lys Gly Ala Glu Val His Arg Leu Ser Asn Glu Lys Val Pro Phe Ala
305 310 315 320

Thr Lys Gly Asn Gln Trp Val Gly Tyr Glu Asp Lys Glu Ser Val Lys
325 330 335

Asn Lys Val Gly Phe Leu Lys Glu Lys Lys Leu Ala Gly Ala Met Val
340 345 350

Trp Ala Leu Asp Leu Asp Asp Phe Gln Gly Thr Cys Gln Pro Lys Glu
355 360 365

Phe Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala
370 375 380

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<212> DNA
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<220>
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<222> (178)..(1689)

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ggtcggtcta gctgcgagga tccgggctgc ccacgaagcg aagggcgggc gcccagg 177
atg gga tgc gtg aag tcc agg ttc ctc cga gat gga agc aag gcc tca 225
Met Gly Cys Val Lys Ser Arg Phe Leu Arg Asp Gly Ser Lys Ala Ser
1 5 10 15
aaa aca gag cca agt gcc aat cag aag ggc cct gtg tat gtg ccg gat 273
Lys Thr Glu Pro Ser Ala Asn Gln Lys Gly Pro Val Tyr Val Pro Asp
20 25 30
ccc acg tcc tcc agc aag ctg gga cca aac aac agc aac agc atg ccc 321
Pro Thr Ser Ser Lys Leu Gly Pro Asn Asn Ser Asn Ser Met Pro
35 40 45
cca ggg ttt gtg gag ggc tct gag gat acc att gtg gtc gca ctg tac 369
Pro Gly Phe Val Glu Gly Ser Glu Asp Thr Ile Val Val Ala Leu Tyr
50 55 60
gac tat gag gct att cac cgt gaa gac ctc agc ttc cag aag gga gac 417
Asp Tyr Glu Ala Ile His Arg Glu Asp Leu Ser Phe Gln Lys Gly Asp
65 70 75 80
cag atg gtg gtt ctg gag gag gct ggg gag tgg tgg aag gca cgg tcc 465
Gln Met Val Val Leu Glu Ala Gly Glu Trp Trp Lys Ala Arg Ser
85 90 95
ctg gct acc aag aag gaa ggc tac atc cca agc aac tat gtg gct cga 513
Leu Ala Thr Lys Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg

100	105	110	
gtt aac tct ttg gag aca gaa gag tgg ttc ttc aag ggg atc agc cg			561
Val Asn Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser Arg			
115	120	125	
aag gat gca gag cgc cac ctc ctg gct cca ggc aac atg ctg ggc tcc			609
Lys Asp Ala Glu Arg His Leu Leu Ala Pro Gly Asn Met Leu Gly Ser			
130	135	140	
ttc atg atc cgg gac agt gag acc acc aaa ggg agc tac tcg ttg tct			657
Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu Ser			
145	150	155	160
gtt cga gac ttt gac ccc cag cac gga gac acc gtg aag cac tat aag			705
Val Arg Asp Phe Asp Pro Gln His Gly Asp Thr Val Lys His Tyr Lys			
165	170	175	
atc cgg acg ctg gac agt gga ggc ttc tac atc tct cca agg agc acc			753
Ile Arg Thr Leu Asp Ser Gly Gly Phe Tyr Ile Ser Pro Arg Ser Thr			
180	185	190	
ttc agc agc ctg cag gaa ctc gtg ctc cac tac aag aag ggg aag gat			801
Phe Ser Ser Leu Gln Glu Leu Val His Tyr Lys Lys Gly Lys Asp			
195	200	205	
ggg ctc tgc cag aag ctg tca gtg ccc tgt gtg tct ccc aaa ccc cag			849
Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Val Ser Pro Lys Pro Gln			
210	215	220	
aag cca tgg gag aaa gat gct tgg gag att cct cga gaa tcc ctc cag			897
Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Gln			
225	230	235	240
atg gag aag aaa ctt gga gct ggg cag ttt gga gaa gtg tgg atg gcc			945
Met Glu Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala			
245	250	255	
acc tac aac aag cac acc aaa gtg gcg gtg aag aca atg aag cca ggg			993
Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly			
260	265	270	
agc atg tcc gtg gag gcc ttc ctg gct gag gcc aac ctg atg aag tcg			1041
Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Ser			
275	280	285	
ctg cag cat gac aaa ctg gtg aag cta cac gct gtg gtc tct cag gag			1089
Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Ser Gln Glu			
290	295	300	
ccc atc ttt att gtc acg gag ttc atg gcc aaa gga agc ctg ctg gac			1137
Pro Ile Phe Ile Val Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp			
305	310	315	320
ttt ctc aag agt gaa gaa ggc agc aag cag cca ctg cca aaa ctc att			1185
Phe Leu Lys Ser Glu Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile			
325	330	335	
gac ttc tca gcc cag atc tca gaa ggc atg gcc ttc att gag cag agg			1233
Asp Phe Ser Ala Gln Ile Ser Glu Gly Met Ala Phe Ile Glu Gln Arg			

340	345	350	
aac tac atc cac cga gac ctg agg gct gcc aac atc tta gtc tct gca Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala 355	360	365	1281
tca ctg gtg tgt aag att gct gac ttt gga ctg gca cga atc atc gag Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Glu 370	375	380	1329
gac aat gag tac aca gct cgg gaa gga gcc aag ttc ccc atc aag tgg Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp 385	390	395	1377
aca gct cct gaa gcc atc aac ttt ggt tcc ttc acc atc aag tca gat Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp 405	410	415	1425
gtc tgg tcc ttt ggt atc ctg ctg atg gaa att gtc acc tat ggc cgg Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg 420	425	430	1473
atc cct tac cca ggt atg tca aac cca gag gtg att cgg gca cta gag Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu 435	440	445	1521
cat ggg tac cgt atg cct cga cca gat aac tgt cca gaa gag ctc tac His Gly Tyr Arg Met Pro Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr 450	455	460	1569
aat atc atg atc cgc tgc tgg aag aac cgc ccc gag gaa cgg ccc acc Asn Ile Met Ile Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr 465	470	475	1617
ttt gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc act gag Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu 485	490	495	1665
agc cag tat cag cag cag cct tga cagcagtaag gacatgagca gagccagaag Ser Gln Tyr Gln Gln Pro 500			1719
ccccatcagt gccttgacac gcccacttg ctggcccac tctcagacac cacaccacac acactgcagc tggtgagtgg gtgggaggac ttccacaatct ctttctgact ctagtcatct gcaatccgcc actctcaggg cctccaagtt ggtatgtctc atttgcctgg aatgactgaa ttcaatctat agctgtgatt taagtggaaa ctgttagaat agtatttaaa taaaagatat gaatgtcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa			1779 1839 1899 1959 2002

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20 25 30

Pro Thr Ser Ser Ser Lys Leu Gly Pro Asn Asn Ser Asn Ser Met Pro
35 40 45

Pro Gly Phe Val Glu Gly Ser Glu Asp Thr Ile Val Val Ala Leu Tyr
50 55 60

Asp Tyr Glu Ala Ile His Arg Glu Asp Leu Ser Phe Gln Lys Gly Asp
65 70 75 80

Gln Met Val Val Leu Glu Glu Ala Gly Glu Trp Trp Lys Ala Arg Ser
85 90 95

Leu Ala Thr Lys Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg
100 105 110

Val Asn Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser Arg
115 120 125

Lys Asp Ala Glu Arg His Leu Leu Ala Pro Gly Asn Met Leu Gly Ser
130 135 140

Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu Ser
145 150 155 160

Val Arg Asp Phe Asp Pro Gln His Gly Asp Thr Val Lys His Tyr Lys
165 170 175

Ile Arg Thr Leu Asp Ser Gly Gly Phe Tyr Ile Ser Pro Arg Ser Thr
180 185 190

Phe Ser Ser Leu Gln Glu Leu Val Leu His Tyr Lys Lys Gly Lys Asp
195 200 205

Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Val Ser Pro Lys Pro Gln
210 215 220

Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Gln
225 230 235 240

Met Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala
245 250 255

Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly
260 265 270

Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Ser
275 280 285

Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Ser Gln Glu
290 295 300

Pro Ile Phe Ile Val Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp
305 310 315 320

Phe Leu Lys Ser Glu Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile
325 330 335

Asp Phe Ser Ala Gln Ile Ser Glu Gly Met Ala Phe Ile Glu Gln Arg
340 345 350

Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala
355 360 365

Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Glu
370 375 380

Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp
385 390 395 400

Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp
405 410 415

Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg
420 425 430

Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu
435 440 445

His Gly Tyr Arg Met Pro Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr
450 455 460

Asn Ile Met Ile Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr
465 470 475 480

Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu
485 490 495

Ser Gln Tyr Gln Gln Gln Pro
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<213> Mouse

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ctgggcaacc agggcgcttc cagacagagt tcctgctgcc acccaccacc cccctctcag 120
cacaggacaa gg atg gag ctc cat ttt ggc tcc tgc ctc tcc ggc tgt ttg 171
Met Glu His Phe Gly Ser Cys Leu Ser Gly Cys Leu
1 5 10
gct ctg ctt gtc ttg ctg cct tcc ctg agc cta gca cag tac gag ggc 219
Ala Leu Leu Val Leu Leu Pro Ser Leu Ser Leu Ala Gln Tyr Glu Gly
15 20 25
tgg ccc tac cag ctc cag tac cct gag tac ttc cag cag ccc gct cct 267
Trp Pro Tyr Gln Leu Gln Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro
30 35 40 45
gag cac cat cag cg^g cag gtg ccc tcc gat gtg gtc aag atc cag gtc 315
Glu His His Gln Arg Gln Val Pro Ser Asp Val Val Lys Ile Gln Val
50 55 60
cgc ctg gc^g ggc cag aag agg aag cac aat gag ggc cgc gtg gag gtc 363
Arg Leu Ala Gly Gln Lys Arg Lys His Asn Glu Gly Arg Val Glu Val
65 70 75
tac tac gaa ggc cag tgg ggc acg gtg tgc gac gat gac ttc tcg atc 411
Tyr Tyr Glu Gly Gln Trp Gly Thr Val Cys Asp Asp Phe Ser Ile
80 85 90
cat gcc gcc cat gtg gtc tgc cgg caa gtg ggc tat gta gag gcc aag 459
His Ala Ala His Val Val Cys Arg Gln Val Gly Tyr Val Glu Ala Lys
95 100 105
tcc tgg gct gcc agc tcc tcc tac ggt cca ggc gaa ggc ccc atc tgg 507
Ser Trp Ala Ala Ser Ser Tyr Gly Pro Gly Glu Gly Pro Ile Trp
110 115 120 125
ttg gac aat atc tac tgt act ggc aaa gag tcg acc ctg gca tct tgc 555
Leu Asp Asn Ile Tyr Cys Thr Gly Lys Glu Ser Thr Leu Ala Ser Cys
130 135 140
tcc tcc aat ggc tgg ggt gtc act gac tgc aag cac act gaa gac gtt 603

Ser Ser Asn Gly Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val			
145	150	155	
gga gtg gtg tgt agt gag aaa aga att cct ggc ttc aaa ttt gac aat			651
Gly Val Val Cys Ser Glu Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn			
160	165	170	
tcg ttg atc aac caa ata gag agc cta aat ata cag gtg gaa gac atc			699
Ser Leu Ile Asn Gln Ile Glu Ser Leu Asn Ile Gln Val Glu Asp Ile			
175	180	185	
cgg att cgg ccc atc ctt tct gcc ttt cgc cat cgc aag cct gtg aca			747
Arg Ile Arg Pro Ile Leu Ser Ala Phe Arg His Arg Lys Pro Val Thr			
190	195	200	205
gag ggc tac gtg gag gtg aag gag ggc aag gct tgg aag cag atc tgc			795
Glu Gly Tyr Val Glu Val Lys Glu Gly Lys Ala Trp Lys Gln Ile Cys			
210	215	220	
aac aaa cac tgg aca gcc aag aat tcc cac gtg gtc tgt ggc atg ttc			843
Asn Lys His Trp Thr Ala Lys Asn Ser His Val Val Cys Gly Met Phe			
225	230	235	
ggc ttc cct gca gag aag acc tac aac ccc aaa gcc tat aaa acc ttt			891
Gly Phe Pro Ala Glu Lys Thr Tyr Asn Pro Lys Ala Tyr Lys Thr Phe			
240	245	250	
gcc tcg cgg agg aag ctg cgt tac tgg aag ttt tct atg aac tgc acg			939
Ala Ser Arg Arg Lys Leu Arg Tyr Trp Lys Phe Ser Met Asn Cys Thr			
255	260	265	
ggc act gaa gcg cat atc tcc agc tgc aag ctg ggc cct tcc gtg acc			987
Gly Thr Glu Ala His Ile Ser Ser Cys Lys Leu Gly Pro Ser Val Thr			
270	275	280	285
cgg gac cct gtg aag aac gcc acc tgt gag aac ggg cag cca gct gtg			1035
Arg Asp Pro Val Lys Asn Ala Thr Cys Glu Asn Gly Gln Pro Ala Val			
290	295	300	
gtc agt tgt gtg cct agc cag atc ttc agc ccc gat gga ccc tca agg			1083
Val Ser Cys Val Pro Ser Gln Ile Phe Ser Pro Asp Gly Pro Ser Arg			
305	310	315	
ttc cgg aaa gcc tac aag cca gag caa ccc ttg gtg cgc ctg aga ggt			1131
Phe Arg Lys Ala Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly			
320	325	330	
gga gcc cag gtc ggg gag ggc cga gtg gag gtg ctg aag aat gga gaa			1179
Gly Ala Gln Val Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu			
335	340	345	
tgg gga acc atc tgc gat gac aag tgg gac ctg gta tct gcc agt gtg			1227
Trp Gly Thr Ile Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val			
350	355	360	365
gtc tgc cga gag ctg ggc ttt ggg acc gct aaa gag gcc atc aca ggc			1275
Val Cys Arg Glu Leu Gly Phe Gly Thr Ala Lys Glu Ala Ile Thr Gly			
370	375	380	
tcc aga cta ggg caa ggg att ggg ccc atc cat ctc aat gaa gtc cag			1323

Ser Arg Leu Gly Gln Gly Ile Gly Pro Ile His Leu Asn Glu Val Gln			
385	390	395	
tgc aca ggg act gag aag tcc atc ata gac tgc aaa ttc aac aca gag			1371
Cys Thr Gly Thr Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Thr Glu			
400	405	410	
tct caa ggc tgc aac cat gaa gaa gat gcc ggg gtg cga tgc aac atc			1419
Ser Gln Gly Cys Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Ile			
415	420	425	
ccc atc atg ggt ttc cag aaa aag gtg cgc ctg aat gga ggc cgc aat			1467
Pro Ile Met Gly Phe Gln Lys Lys Val Arg Leu Asn Gly Gly Arg Asn			
430	435	440	445
cct tat gag ggc cga gtg gag gtg cta aca gag aga aat ggg tcc ctt			1515
Pro Tyr Glu Gly Arg Val Glu Val Leu Thr Glu Arg Asn Gly Ser Leu			
450	455	460	
gtt tgg ggg act gta tgc ggc cag aac tgg ggc att gtg gaa gcc atg			1563
Val Trp Gly Thr Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met			
465	470	475	
gtg gtc tgc cgg cag cta ggc ctg ggc ttt gcc agc aat gcc ttt cag			1611
Val Val Cys Arg Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln			
480	485	490	
gag acc tgg tac tgg cat gga aat atc ttc gcc aac aac gtg gtc atg			1659
Glu Thr Trp Tyr Trp His Gly Asn Ile Phe Ala Asn Asn Val Val Met			
495	500	505	
agt gga gtg aag tgc tca gga acg gag ctg tcc cta gca cac tgc cgc			1707
Ser Gly Val Lys Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg			
510	515	520	525
cat gac gag gag gtg gcc tgc ccc gag ggc ggg gtg cgg ttt ggt gct			1755
His Asp Glu Glu Val Ala Cys Pro Glu Gly Gly Val Arg Phe Gly Ala			
530	535	540	
gga gtc gcc tgc tcg gaa act gca cct gac ctg gtg ctt aat gct gag			1803
Gly Val Ala Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu			
545	550	555	
att gtc cag cag act gcc tac ctg gag gac agg ccc atg tcc ttg ctg			1851
Ile Val Gln Gln Thr Ala Tyr Leu Glu Asp Arg Pro Met Ser Leu Leu			
560	565	570	
cag tgt gcc atg gag gag aac tgc ctc tcc gcc tcc gct gtg cac acc			1899
Gln Cys Ala Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Val His Thr			
575	580	585	
gac ccc acc aga ggc cac cgg cgc ctt tta cgc ttc tcc tcc cag atc			1947
Asp Pro Thr Arg Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile			
590	595	600	605
cac aac aat ggc cag tct gac ttc cgc ccc aag aat ggc cgc cat gcg			1995
His Asn Asn Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala			
610	615	620	
tgg att tgg cac gac tgc cac agg cac tac cac agc atg gaa gtc ttc			2043

Trp Ile Trp His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe		
625	630	635
act tac tat gac ctg ctg agc ctc aac ggc acc aag gtg gct gag ggc		2091
Thr Tyr Asp Leu Leu Ser Leu Asn Gly Thr Lys Val Ala Glu Gly		
640	645	650
cac aag gcc agc ttc tgc ctg gag gac act gag tgt gag gga gac att		2139
His Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile		
655	660	665
cag aag agt tac gag tgt gcc aac ttt gga gaa caa ggc atc acc atg		2187
Gln Lys Ser Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Met		
670	675	680
ggc tgc tgg gac atg tac cgt cat gac att gac tgc cag tgg ata gac		2235
Gly Cys Trp Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp		
690	695	700
atc acc gat gtg ccc cct gga gac tac ctg ttc cag gtt gtc att aac		2283
Ile Thr Asp Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn		
705	710	715
ccc aac tat gaa gtg cca gaa tca gat ttc tct aac aac atc atg aag		2331
Pro Asn Tyr Glu Val Pro Glu Ser Asp Phe Ser Asn Asn Ile Met Lys		
720	725	730
tgc agg agc cgc tat gat ggc tac cgc atc tgg atg tac aac tgt cac		2379
Cys Arg Ser Arg Tyr Asp Gly Tyr Arg Ile Trp Met Tyr Asn Cys His		
735	740	745
gta ggt gga gcc ttc agt gag gag aca gaa cag aag ttc gaa cac ttc		2427
Val Gly Gly Ala Phe Ser Glu Glu Thr Glu Gln Lys Phe Glu His Phe		
750	755	760
765		
agt gga ctt cta aat aac cag ctc tct gta cag taa agaagatcct		2473
Ser Gly Leu Leu Asn Asn Gln Leu Ser Val Gln		
770	775	
gggccaggca tgatggctca tgcctgtaat ccctgcactc atgctgaggc aggaggatg		2533
ccacaagatt tccactctgg acattaaacc aagcttcagt ttcaaaagaa atgaatgaaa		2593
gaaaggaagg aaggaaggaa ggaaggaagg aaggaaggaa ggaaggaagg aagaaagggg		2653
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35 40 45

Gln Arg Gln Val Pro Ser Asp Val Val Lys Ile Gln Val Arg Leu Ala
50 55 60

Gly Gln Lys Arg Lys His Asn Glu Gly Arg Val Glu Val Tyr Tyr Glu
65 70 75 80

Gly Gln Trp Gly Thr Val Cys Asp Asp Phe Ser Ile His Ala Ala
85 90 95

His Val Val Cys Arg Gln Val Gly Tyr Val Glu Ala Lys Ser Trp Ala
100 105 110

Ala Ser Ser Ser Tyr Gly Pro Gly Glu Gly Pro Ile Trp Leu Asp Asn
115 120 125

Ile Tyr Cys Thr Gly Lys Glu Ser Thr Leu Ala Ser Cys Ser Ser Asn
130 135 140

Gly Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val
145 150 155 160

Cys Ser Glu Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile
165 170 175

Asn Gln Ile Glu Ser Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg
180 185 190

Pro Ile Leu Ser Ala Phe Arg His Arg Lys Pro Val Thr Glu Gly Tyr
195 200 205

Val Glu Val Lys Glu Gly Lys Ala Trp Lys Gln Ile Cys Asn Lys His

210

215

220

Trp Thr Ala Lys Asn Ser His Val Val Cys Gly Met Phe Gly Phe Pro
225 230 235 240

Ala Glu Lys Thr Tyr Asn Pro Lys Ala Tyr Lys Thr Phe Ala Ser Arg
245 250 255

Arg Lys Leu Arg Tyr Trp Lys Phe Ser Met Asn Cys Thr Gly Thr Glu
260 265 270

Ala His Ile Ser Ser Cys Lys Leu Gly Pro Ser Val Thr Arg Asp Pro
275 280 285

Val Lys Asn Ala Thr Cys Glu Asn Gly Gln Pro Ala Val Val Ser Cys
290 295 300

Val Pro Ser Gln Ile Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys
305 310 315 320

Ala Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Gln
325 330 335

Val Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr
340 345 350

Ile Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg
355 360 365

Glu Leu Gly Phe Gly Thr Ala Lys Glu Ala Ile Thr Gly Ser Arg Leu
370 375 380

Gly Gln Gly Ile Gly Pro Ile His Leu Asn Glu Val Gln Cys Thr Gly
385 390 395 400

Thr Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Thr Glu Ser Gln Gly
405 410 415

Cys Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Ile Pro Ile Met
420 425 430

Gly Phe Gln Lys Lys Val Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu
435 440 445

Gly Arg Val Glu Val Leu Thr Glu Arg Asn Gly Ser Leu Val Trp Gly

450

455

460

Thr Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys
465 470 475 480

Arg Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp
485 490 495

Tyr Trp His Gly Asn Ile Phe Ala Asn Asn Val Val Met Ser Gly Val
500 505 510

Lys Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Glu
515 520 525

Glu Val Ala Cys Pro Glu Gly Gly Val Arg Phe Gly Ala Gly Val Ala
530 535 540

Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Ile Val Gln
545 550 555 560

Gln Thr Ala Tyr Leu Glu Asp Arg Pro Met Ser Leu Leu Gln Cys Ala
565 570 575

Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Val His Thr Asp Pro Thr
580 585 590

Arg Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn
595 600 605

Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp
610 615 620

His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe Thr Tyr Tyr
625 630 635 640

Asp Leu Leu Ser Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala
645 650 655

Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Ser
660 665 670

Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Met Gly Cys Trp
675 680 685

Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp

690

695

700

Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Tyr
705 710 715 720

Glu Val Pro Glu Ser Asp Phe Ser Asn Asn Ile Met Lys Cys Arg Ser
725 730 735

Arg Tyr Asp Gly Tyr Arg Ile Trp Met Tyr Asn Cys His Val Gly Gly
740 745 750

Ala Phe Ser Glu Glu Thr Glu Gln Lys Phe Glu His Phe Ser Gly Leu
755 760 765

Leu Asn Asn Gln Leu Ser Val Gln
770 775

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caggagacta agcagataaa aggagcc atg act tct ggc gct agt cat atg ctg 120
Met Thr Ser Gly Ala Ser His Met Leu
1 5

gaa gct gcc ctg gag cag atg gac ggg atc att gca ggc act aaa aca 174
Glu Ala Ala Leu Glu Gln Met Asp Gly Ile Ile Ala Gly Thr Lys Thr 222
10 15 20 25

gct gca gat ttt agt gat ggt acc tgt gag cct ggg ctg tct ccc cca 270
Ala Ala Asp Phe Ser Asp Gly Thr Cys Glu Pro Gly Leu Ser Pro Pro
30 35 40

tcc acc tgc ttg aac tcc atg cct gtg ctc cat ctc att gag gac ctg 318
Ser Thr Cys Leu Asn Ser Met Pro Val Leu His Leu Ile Glu Asp Leu
45 50 55

aga cta gcc ttg gag atg ttg gca ctt cct cag gaa aga gaa gcc ctc 366
Arg Leu Ala Leu Glu Met Leu Ala Leu Pro Gln Glu Arg Glu Ala Leu
60 65 70

ctg agc cag gtc cct ggc cca aca gct acc tac ata aag gag tgg ttt 414
Leu Ser Gln Val Pro Gly Pro Thr Ala Thr Tyr Ile Lys Glu Trp Phe

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75

80

85

gag gac agc ttg tcc cag gta aat cac cac ggt gct gct agt aat gaa			462
Glu Asp Ser Leu Ser Gln Val Asn His His Gly Ala Ala Ser Asn Glu			
90	95	100	105
acc tac cag gaa cgc ctg gca cgg cta gaa gga gat aaa gag tcc ctc			510
Thr Tyr Gln Glu Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser Leu			
110	115	120	
ata cta cag gtg agc gtc ctc aca gat caa gtg gaa gcc caa gga gag			558
Ile Leu Gln Val Ser Val Leu Thr Asp Gln Val Glu Ala Gln Gly Glu			
125	130	135	
aag att cgg gac ctt gaa gtg tgt ctg gaa ggc cac cag gtg aag ctc			606
Lys Ile Arg Asp Leu Glu Val Cys Leu Glu Gly His Gln Val Lys Leu			
140	145	150	
aat gct gca gaa gag atg ctt cag cag gag ctg cta agt cgc aca tct			654
Asn Ala Ala Glu Glu Met Leu Gln Gln Glu Leu Leu Ser Arg Thr Ser			
155	160	165	
ctg gag acc cag aag ttg gat ctg atg act gag gtg tct gag ctg aag			702
Leu Glu Thr Gln Lys Leu Asp Leu Met Thr Glu Val Ser Glu Leu Lys			
170	175	180	185
ctc aag ctg gtt ggt atg gaa aaa gaa cag aaa gaa caa gaa gaa aaa			750
Leu Lys Leu Val Gly Met Glu Lys Glu Gln Lys Glu Gln Glu Glu Lys			
190	195	200	
cag aga aaa gca gag gag tta ctg caa gag ctt aag cac ctc aaa atc			798
Gln Arg Lys Ala Glu Glu Leu Leu Gln Glu Leu Lys His Leu Lys Ile			
205	210	215	
aag gtg gag gag ctg gag aac gag cgg aac cag tat gag tgg gag ctg			846
Lys Val Glu Glu Leu Glu Asn Glu Arg Asn Gln Tyr Glu Trp Glu Leu			
220	225	230	
aag gcc acc aag gct gag gta gcc cag ctg caa gaa cag gtg gcc cta			894
Lys Ala Thr Lys Ala Glu Val Ala Gln Leu Gln Glu Gln Val Ala Leu			
235	240	245	
aaa gat gca gaa att gag cgt ctc cac agc cag ctc tcc cgg agt gca			942
Lys Asp Ala Glu Ile Glu Arg Leu His Ser Gln Leu Ser Arg Ser Ala			
250	255	260	265
gct ctc cac agc gac cat gca gag cga gat caa gaa atc cac cgt ctg			990
Ala Leu His Ser Asp His Ala Glu Arg Asp Gln Glu Ile His Arg Leu			
270	275	280	
aaa atg ggg atg gaa aca ctg ctg gtt gcc aat gag gat aag gac cgt			1038
Lys Met Gly Met Glu Thr Leu Leu Val Ala Asn Glu Asp Lys Asp Arg			
285	290	295	
cgg ata gag gag ctg aca ggg ctg ttg aac aag tac cta agg gta aag			1086
Arg Ile Glu Glu Leu Thr Gly Leu Leu Asn Lys Tyr Leu Arg Val Lys			
300	305	310	
gag att gtg atg gca act cag ggg cct tca gaa aga acc ctc tcc atc			1134
Glu Ile Val Met Ala Thr Gln Gly Pro Ser Glu Arg Thr Leu Ser Ile			

315

320

325

aat gaa gat gaa ata gag gga agc ttc cga aaa tgg aat acc aca aat Asn Glu Asp Glu Ile Glu Gly Ser Phe Arg Lys Trp Asn Thr Thr Asn 330 335 340 345	1182
aaa agc cca gag gaa gtc ccg aag caa gag ata tca cca cga tgc agc Lys Ser Pro Glu Glu Val Pro Lys Gln Glu Ile Ser Pro Arg Cys Ser 350 355 360	1230
tct ccc acc cca gga cca cct cct ttg cca cag aaa tca ctg gag agc Ser Pro Thr Pro Gly Pro Pro Leu Pro Gln Lys Ser Leu Glu Ser 365 370 375	1278
agg gct cag aag aaa ctc tcc tgc agt cta gaa gac ttg aga cgt gaa Arg Ala Gln Lys Lys Leu Ser Cys Ser Leu Glu Asp Leu Arg Arg Glu 380 385 390	1326
tct ggg gat aag tgt gtc gat ggg aac cag ctg tcc cca gtg gga gag Ser Gly Asp Lys Cys Val Asp Gly Asn Gln Leu Ser Pro Val Gly Glu 395 400 405	1374
ccc aag gac agc tct ttc cta gcg gag cag aaa tac ccc aca tta cct Pro Lys Asp Ser Ser Phe Leu Ala Glu Gln Lys Tyr Pro Thr Leu Pro 410 415 420 425	1422
ggg aag ctt tca gga gcc aca ccc aat gga gaa gct gcc aaa tct cct Gly Lys Leu Ser Gly Ala Thr Pro Asn Gly Glu Ala Ala Lys Ser Pro 430 435 440	1470
ccc act gcc tcc ctc cag cct gac tct tca ggg agc agc cag cca aag Pro Thr Ala Ser Leu Gln Pro Asp Ser Ser Gly Ser Ser Gln Pro Lys 445 450 455	1518
ctg aga gac aca gaa gga ggc tgg gaa gat ata gtc tca tct gct tcg Leu Arg Asp Thr Glu Gly Gly Trp Glu Asp Ile Val Ser Ser Ala Ser 460 465 470	1566
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cag tct gga aac ttc aat act gat gca ccg ggg atg gca gag ttt cga Gln Ser Gly Asn Phe Asn Thr Asp Ala Pro Gly Met Ala Glu Phe Arg 510 515 520	1710
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gac acc aag gga cag aaa tgt gat gcc aat gcc ccc ttt gcc cag tgg Asp Thr Lys Gly Gln Lys Cys Asp Ala Asn Ala Pro Phe Ala Gln Trp 540 545 550	1806
agc aca gaa cgc gta tgt aca tgg atg gag gat ttc ggc ctg ggt cag Ser Thr Glu Arg Val Cys Thr Trp Met Glu Asp Phe Gly Leu Gly Gln	1854

555

560

565

tat	gtg	atc	ttt	gcc	aga	cag	tgg	gtg	aca	tct	gga	cat	aca	cta	ctg		1902
Tyr	Val	Ile	Phe	Ala	Arg	Gln	Trp	Val	Thr	Ser	Gly	His	Thr	Leu	Leu		
570				575					580					585			
aca	gct	acc	cct	cag	gac	atg	gaa	aag	gag	cta	ggg	att	aaa	cac	ccc		1950
Thr	Ala	Thr	Pro	Gln	Asp	Met	Glu	Lys	Glu	Leu	Gly	Ile	Lys	His	Pro		
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ctc	cac	agg	aag	ctg	gtt	tta	gca	gtg	aaa	gct	atc	aac	gcc	aag		1998	
Leu	His	Arg	Lys	Lys	Leu	Val	Leu	Ala	Val	Lys	Ala	Ile	Asn	Ala	Lys		
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caa	gaa	gaa	acg	tct	gcg	ctg	gac	cac	att	tgg	gtg	aca	cgg	tgg		2046	
Gln	Glu	Thr	Ser	Ala	Leu	Leu	Asp	His	Ile	Trp	Val	Thr	Arg	Trp			
				620			625			630							
ctt	gat	gat	att	ggc	tta	ccc	caa	tac	aaa	gac	cag	ttt	cat	gaa	tca		2094
Leu	Asp	Asp	Ile	Gly	Leu	Pro	Gln	Tyr	Lys	Asp	Gln	Phe	His	Glu	Ser		
				635			640			645							
aga	gtt	gat	ggg	cga	atg	ctg	caa	tac	cta	act	gtg	aat	gat	cta	ctc		2142
Arg	Val	Asp	Gly	Arg	Met	Leu	Gln	Tyr	Leu	Thr	Val	Asn	Asp	Leu	Leu		
				650			655			660			665				
ttc	tta	aaa	gtc	acc	agc	caa	cta	cat	cat	ctc	agc	atc	aaa	tgt	gtc		2190
Phe	Leu	Lys	Val	Thr	Ser	Gln	Leu	His	His	Leu	Ser	Ile	Lys	Cys	Ala		
				670			675			680							
att	cac	gtg	cta	cat	gtc	aac	aag	ttc	aac	ccc	aac	tgc	ctg	cac	agg		2238
Ile	His	Val	Leu	His	Val	Asn	Lys	Phe	Asn	Pro	Asn	Cys	Leu	His	Arg		
				685			690			695							
agg	cct	gct	gat	gag	agt	aac	ttc	tcc	cct	tcc	gaa	gtt	gtg	cag	tgg		2286
Arg	Pro	Ala	Asp	Glu	Ser	Asn	Leu	Ser	Pro	Ser	Glu	Val	Val	Gln	Trp		
				700			705			710							
tcc	aac	cac	agg	gta	atg	gag	tgg	ctg	cga	tcc	gtg	gac	ctg	gca	gag		2334
Ser	Asn	His	Arg	Val	Met	Glu	Trp	Leu	Arg	Ser	Val	Asp	Leu	Ala	Glu		
				715			720			725							
tat	gca	ccc	aac	ctt	cga	ggg	agt	ggc	gtc	cat	ggc	ggc	ctc	att	atc		2382
Tyr	Ala	Pro	Asn	Leu	Arg	Gly	Ser	Gly	Val	His	Gly	Gly	Leu	Ile	Ile		
				730			735			740			745				
ctg	gag	cct	cgc	ttt	act	ggg	gac	acc	ctg	gct	atg	ctt	ctt	aac	atc		2430
Leu	Glu	Pro	Arg	Phe	Thr	Gly	Asp	Thr	Leu	Ala	Met	Leu	Leu	Asn	Ile		
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ccc	cca	cag	aag	acg	ctc	ctc	agg	cgc	cat	ctg	acc	acc	aag	ttc	aac		2478
Pro	Pro	Gln	Lys	Thr	Leu	Leu	Arg	Arg	His	Leu	Thr	Thr	Lys	Phe	Asn		
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gcc	ctg	att	ggt	cct	gag	gct	gaa	cag	gaa	aag	cga	gac	aaa	atg	gcc		2526
Ala	Leu	Ile	Gly	Pro	Glu	Ala	Glu	Gln	Glu	Lys	Arg	Asp	Lys	Met	Ala		
				780			785			790							
tca	ccc	gcc	tac	aca	cct	ctg	acc	acc	acc	gcc	aaa	gtt	cgg	cct	agg		2574
Ser	Pro	Ala	Tyr	Thr	Pro	Leu	Thr	Thr	Ala	Lys	Val	Arg	Pro	Arg			

795

800

805

aaa ctt gga ttt tca cat ttt gga aac atg aga aaa aag aag ttt gat			2622
Lys Leu Gly Phe Ser His Phe Gly Asn Met Arg Lys Lys Lys Phe Asp			
810	815	820	825
gaa tct aca gat tac att tgc ccc atg gag cct gga gat gct gtc agt			2670
Glu Ser Thr Asp Tyr Ile Cys Pro Met Glu Pro Gly Asp Ala Val Ser			
830	835	840	
gac agc cac agg gtc tac gga gtc tac cgg ggc ctc agt ccc ctt gac			2718
Asp Ser His Arg Val Tyr Gly Val Tyr Arg Gly Leu Ser Pro Leu Asp			
845	850	855	
aac cat gaa cta gat ggt ttg gac cag gtg gga cag ata agc tga			2763
Asn His Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser			
860	865	870	
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gccctggta atcgcaaaag gttcagtct cagacgctgc ccctattctt cagtcgaggg			3123
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20	25	30

Thr Cys Glu Pro Gly Leu Ser Pro Pro Ser Thr Cys Leu Asn Ser Met		
35	40	45

Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu Glu Met Leu		
50	55	60

Ala Leu Pro Gln Glu Arg Glu Ala Leu Leu Ser Gln Val Pro Gly Pro
65 70 75 80

Thr Ala Thr Tyr Ile Lys Glu Trp Phe Glu Asp Ser Leu Ser Gln Val
85 90 95

Asn His His Gly Ala Ala Ser Asn Glu Thr Tyr Gln Glu Arg Leu Ala
100 105 110

Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val Ser Val Leu
115 120 125

Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Val
130 135 140

Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu Glu Met Leu
145 150 155 160

Gln Gln Glu Leu Leu Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp
165 170 175

Leu Met Thr Glu Val Ser Glu Leu Lys Leu Lys Leu Val Gly Met Glu
180 185 190

Lys Glu Gln Lys Glu Gln Glu Glu Lys Gln Arg Lys Ala Glu Glu Leu
195 200 205

Leu Gln Glu Leu Lys His Leu Lys Ile Lys Val Glu Glu Leu Glu Asn
210 215 220

Glu Arg Asn Gln Tyr Glu Trp Glu Leu Lys Ala Thr Lys Ala Glu Val
225 230 235 240

Ala Gln Leu Gln Glu Gln Val Ala Leu Lys Asp Ala Glu Ile Glu Arg
245 250 255

Leu His Ser Gln Leu Ser Arg Ser Ala Ala Leu His Ser Asp His Ala
260 265 270

Glu Arg Asp Gln Glu Ile His Arg Leu Lys Met Gly Met Glu Thr Leu
275 280 285

Leu Val Ala Asn Glu Asp Lys Asp Arg Arg Ile Glu Glu Leu Thr Gly
290 295 300

Leu Leu Asn Lys Tyr Leu Arg Val Lys Glu Ile Val Met Ala Thr Gln
305 310 315 320

Gly Pro Ser Glu Arg Thr Leu Ser Ile Asn Glu Asp Glu Ile Glu Gly
325 330 335

Ser Phe Arg Lys Trp Asn Thr Thr Asn Lys Ser Pro Glu Glu Val Pro
340 345 350

Lys Gln Glu Ile Ser Pro Arg Cys Ser Ser Pro Thr Pro Gly Pro Pro
355 360 365

Pro Leu Pro Gln Lys Ser Leu Glu Ser Arg Ala Gln Lys Lys Leu Ser
370 375 380

Cys Ser Leu Glu Asp Leu Arg Arg Glu Ser Gly Asp Lys Cys Val Asp
385 390 395 400

Gly Asn Gln Leu Ser Pro Val Gly Glu Pro Lys Asp Ser Ser Phe Leu
405 410 415

Ala Glu Gln Lys Tyr Pro Thr Leu Pro Gly Lys Leu Ser Gly Ala Thr
420 425 430

Pro Asn Gly Glu Ala Ala Lys Ser Pro Pro Thr Ala Ser Leu Gln Pro
435 440 445

Asp Ser Ser Gly Ser Ser Gln Pro Lys Leu Arg Asp Thr Glu Gly Gly
450 455 460

Trp Glu Asp Ile Val Ser Ser Ala Ser Ser Gly Thr Glu Ser Ser Pro
465 470 475 480

Gln Ser Pro Val Thr Pro Asp Gly Lys Arg Ser Pro Lys Gly Ile Lys
485 490 495

Lys Phe Trp Gly Lys Ile Arg Arg Thr Gln Ser Gly Asn Phe Asn Thr
500 505 510

Asp Ala Pro Gly Met Ala Glu Phe Arg Arg Gly Gly Leu Arg Ala Thr
515 520 525

Ala Gly Pro Arg Leu Ser Arg Thr Arg Asp Thr Lys Gly Gln Lys Cys
530 535 540

Asp Ala Asn Ala Pro Phe Ala Gln Trp Ser Thr Glu Arg Val Cys Thr
545 550 555 560

Trp Met Glu Asp Phe Gly Leu Gly Gln Tyr Val Ile Phe Ala Arg Gln
565 570 575

Trp Val Thr Ser Gly His Thr Leu Leu Thr Ala Thr Pro Gln Asp Met
580 585 590

Glu Lys Glu Leu Gly Ile Lys His Pro Leu His Arg Lys Lys Leu Val
595 600 605

Leu Ala Val Lys Ala Ile Asn Ala Lys Gln Glu Glu Thr Ser Ala Leu
610 615 620

Leu Asp His Ile Trp Val Thr Arg Trp Leu Asp Asp Ile Gly Leu Pro
625 630 635 640

Gln Tyr Lys Asp Gln Phe His Glu Ser Arg Val Asp Gly Arg Met Leu
645 650 655

Gln Tyr Leu Thr Val Asn Asp Leu Leu Phe Leu Lys Val Thr Ser Gln
660 665 670

Leu His His Leu Ser Ile Lys Cys Ala Ile His Val Leu His Val Asn
675 680 685

Lys Phe Asn Pro Asn Cys Leu His Arg Arg Pro Ala Asp Glu Ser Asn
690 695 700

Leu Ser Pro Ser Glu Val Val Gln Trp Ser Asn His Arg Val Met Glu
705 710 715 720

Trp Leu Arg Ser Val Asp Leu Ala Glu Tyr Ala Pro Asn Leu Arg Gly
725 730 735

Ser Gly Val His Gly Gly Leu Ile Ile Leu Glu Pro Arg Phe Thr Gly
740 745 750

Asp Thr Leu Ala Met Leu Leu Asn Ile Pro Pro Gln Lys Thr Leu Leu
755 760 765

Arg Arg His Leu Thr Thr Lys Phe Asn Ala Leu Ile Gly Pro Glu Ala
770 775 780

Glu Gln Glu Lys Arg Asp Lys Met Ala Ser Pro Ala Tyr Thr Pro Leu
785 790 795 800

Thr Thr Thr Ala Lys Val Arg Pro Arg Lys Leu Gly Phe Ser His Phe
805 810 815

Gly Asn Met Arg Lys Lys Phe Asp Glu Ser Thr Asp Tyr Ile Cys
820 825 830

Pro Met Glu Pro Gly Asp Ala Val Ser Asp Ser His Arg Val Tyr Gly
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865 870

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Met
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Arg Trp Leu Leu Pro Trp Thr Leu Ala Ala Val Ala Val Leu Arg Val
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Gly Asn Ile Leu Ala Thr Ala Leu Ser Pro Thr Pro Thr Met Thr
20 25 30

ttc acc cca gca cca cta gag gaa acg act aca cgc ccc gaa ttc tgc 320
Phe Thr Pro Ala Pro Leu Glu Glu Thr Thr Arg Pro Glu Phe Cys
35 40 45

aag tgg cca tgt gag tgc cca caa tcc cca cct cgc tgc cca ctg ggc 368
Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu Gly
50 55 60 65

gtc agc cta atc aca gat ggc tgt gaa tgc tgt aag ata tgt gcc cag 416

Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Ile Cys Ala Gln			
70	75	80	
cag ctt ggg gac aac tgc aca gag gct gcc atc tgt gac cca cac cgg Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His Arg			464
85	90	95	
ggc ctc tac tgc gat tac agt ggg gat cgc ccg agg tac gca ata gga Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile Gly			512
100	105	110	
gtg tgt gca cag gtg gtc ggt gtg ggc tgt gtc ctg gat ggc gta cgc Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val Arg			560
115	120	125	
tac acc aat ggc gag tcc ttc caa ccc aac tgc agg tac aac tgt acc Tyr Thr Asn Gly Glu Ser Phe Gln Pro Asn Cys Arg Tyr Asn Cys Thr			608
130	135	140	145
tgc att gat ggc acg gtg ggc tgc aca ccg ctg tgc cta agc ccc agg Cys Ile Asp Gly Thr Val Gly Cys Thr Pro Leu Cys Leu Ser Pro Arg			656
150	155	160	
ccc cca cgc ctc tgg tgc cgc cag ccc ccg cac gtg aga gtc cct ggc Pro Pro Arg Leu Trp Cys Arg Gln Pro Arg His Val Arg Val Pro Gly			704
165	170	175	
cag tgc tgt gag cag tgg gtg tgt gat gat gac gca agg aga cca cgc Gln Cys Cys Glu Gln Trp Val Cys Asp Asp Ala Arg Arg Pro Arg			752
180	185	190	
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195	200	205	
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210	215	220	225
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230	235	240	
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245	250	255	
cca tgt gat gtg gac atc caa cta cac atc aag gca ggg aag aaa tgc Pro Cys Asp Val Asp Ile Gln Leu His Ile Lys Ala Gly Lys Lys Cys			992
260	265	270	
ctg gct gtg tac cag cca gag gag gcc acg aac ttc act ctc gca ggc Leu Ala Val Tyr Gln Pro Glu Glu Ala Thr Asn Phe Thr Leu Ala Gly			1040
275	280	285	
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290	295	300	305
gac aat agg tgt tgc atc ccc tac aag tcc aag acc atc agt gtg gat			1136

Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Ser Val Asp		
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340	345	350
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35 40 45

Cys Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu
50 55 60

Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Ile Cys Ala
65 70 75 80

Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
85 90 95

Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
100 105 110

Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
115 120 125

Arg Tyr Thr Asn Gly Glu Ser Phe Gln Pro Asn Cys Arg Tyr Asn Cys
130 135 140

Thr Cys Ile Asp Gly Thr Val Gly Cys Thr Pro Leu Cys Leu Ser Pro
145 150 155 160

Arg Pro Pro Arg Leu Trp Cys Arg Gln Pro Arg His Val Arg Val Pro
165 170 175

Gly Gln Cys Cys Glu Gln Trp Val Cys Asp Asp Asp Ala Arg Arg Pro
180 185 190

Arg Gln Thr Ala Leu Leu Asp Thr Arg Ala Phe Ala Ala Ser Gly Ala
195 200 205

Val Glu Gln Arg Tyr Glu Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
210 215 220

Pro Cys Ser Thr Thr Cys Gly Leu Gly Ile Ser Thr Arg Ile Ser Asn
225 230 235 240

Val Asn Ala Arg Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
245 250 255

Arg Pro Cys Asp Val Asp Ile Gln Leu His Ile Lys Ala Gly Lys Lys
260 265 270

Cys Leu Ala Val Tyr Gln Pro Glu Glu Ala Thr Asn Phe Thr Leu Ala
275 280 285

Gly Cys Val Ser Thr Arg Thr Tyr Arg Pro Lys Tyr Cys Gly Val Cys
290 295 300

Thr Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Ser Val
305 310 315 320

Asp Phe Gln Cys Pro Glu Gly Pro Gly Phe Ser Arg Gln Val Leu Trp
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 Met Leu Val Met Lys Leu Phe Thr Cys Phe Leu
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 Gln Val Ala Gly Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala
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 Gly Asn Asn Ser Thr Glu Val Glu Val Val Pro Phe Asn Glu Val Trp
 30 35 40

 ggt cgc agc tac tgt cgg ccc atg gag aag ctg gtg tac atc ttg gat 494
 Gly Arg Ser Tyr Cys Arg Pro Met Glu Lys Leu Val Tyr Ile Leu Asp
 45 50 55

 gaa tac cct gat gag gtg tct cac ata ttc agt ccg tcc tgt gtc ctt 542
 Glu Tyr Pro Asp Glu Val Ser His Ile Phe Ser Pro Ser Cys Val Leu
 60 65 70 75

 ctg agt cgc tgt agt ggc tgc tgt ggt gat gaa ggt ctg cac tgt gtg 590
 Leu Ser Arg Cys Ser Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val
 80 85 90

 ccg ata aag aca gcc aac atc act atg cag atc ttg aag att ccc ccc 638
 Pro Ile Lys Thr Ala Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro
 95 100 105

 aat cgg gat cca cat ttc tat gtg gag atg aca ttt tct cag gat gtg 686
 Asn Arg Asp Pro His Phe Tyr Val Glu Met Thr Phe Ser Gln Asp Val
 110 115 120

 ctc tgt gaa tgc aga cct att ctg gag acg aca aag gca gaa agg agg 734
 Leu Cys Glu Cys Arg Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg
 125 130 135

 aaa acc aag ggg aag agg aag agg agt aga aac tca cag act gag gaa 782
 Lys Thr Lys Gly Lys Arg Lys Arg Ser Arg Asn Ser Gln Thr Glu Glu

140	145	150	155	
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gcatggaagg acaagacgct caggaattca	gtgccttaaa acagaacgag	agagaaaagaa		1014
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Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr				
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Glu Val Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys				
35 40 45				
Arg Pro Met Glu Lys Leu Val Tyr Ile Leu Asp Glu Tyr Pro Asp Glu				
50 55 60				
Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser				
65 70 75 80				

Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Pro Ile Lys Thr Ala
85 90 95

Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
100 105 110

Phe Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
115 120 125

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ccacttaaag aaaccctttt accggcaaac ctatgctaaa gagtataagt aacaaaggaa 180
accaaacagt tatctgtcaa gtaacaagca ttaatgaca ga atg gct cac ctt 234
Met Ala His Leu
1
aag cga cta gta aaa ttg cac att aaa aga cat tac cac aga aag ttc 282
Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr His Arg Lys Phe
5 10 15 20
tgg aag ctg ggt gca gtc atc ttt ttc ttt tta gta gtt ctg att tta 330
Trp Lys Leu Gly Ala Val Ile Phe Phe Leu Val Val Leu Ile Leu
25 30 35
atg caa aga gaa gta agt gtt cag tat tcc aag gag gaa tca aag atg 378
Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu Glu Ser Lys Met
40 45 50
gag agg aac ttg aaa aac aaa aac aaa atg ttg gat ttt atg ctc gaa 426
Glu Arg Asn Leu Lys Asn Lys Asn Lys Met Leu Asp Phe Met Leu Glu
55 60 65
gct gta aat aat att aaa gat gca atg cca aag atg caa ata gga gcg 474
Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met Gln Ile Gly Ala
70 75 80

ccc att aag gag aat atc gac gtc cgc gag aga ccc tgg ctg caa ggg Pro Ile Lys Glu Asn Ile Asp Val Arg Glu Arg Pro Cys Leu Gln Gly 85 90 95 100	522
tac tac aca gcc gcg gag ttg aag ccg gtt ttt gat cgc cca cct cag Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Phe Asp Arg Pro Pro Gln 105 110 115	570
gat tct aac gca cct ggt gct tct ggc aag ccg ttt aag atc acc cac Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Pro Phe Lys Ile Thr His 120 125 130	618
ctc agc ccg gag gag cag aag gag aaa gag cga ggg gaa acg aag cac Leu Ser Pro Glu Glu Gln Lys Glu Lys Glu Arg Gly Glu Thr Lys His 135 140 145	666
tgc ttc aac gcc ttt gca agt gac aga att tct ctg cac cgg gac ctt Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu His Arg Asp Leu 150 155 160	714
ggg cct gac acc cga cca cct gaa tgt att gaa caa aaa ttt aag cgc Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln Lys Phe Lys Arg 165 170 175 180	762
tgc ccg ccc ctg cct acc acc agt gtc ata ata gtc ttt cac aat gaa Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val Phe His Asn Glu 185 190 195	810
gca tgg tcc acg ctg ctt agg acc gtc cac agt gtg ctc tat tct tca Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Leu Tyr Ser Ser 200 205 210	858
cct gcc ata ctg ctg aag gag atc att ttg gtg gat gat gct agt gta Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp Asp Ala Ser Val 215 220 225	906
gac gac tac ctg cat gaa aag ctg gag gaa tac ata aaa cag ttt tct Asp Asp Tyr Leu His Glu Lys Leu Glu Glu Tyr Ile Lys Gln Phe Ser 230 235 240	954
att gtg aaa ata gtc agg cag caa gaa agg aaa ggc ctg atc acc gcg Ile Val Lys Ile Val Arg Gln Gln Glu Arg Lys Gly Leu Ile Thr Ala 245 250 255 260	1002
cgg ttg cta ggg gca gct gta gca act gcc gag acg ctc acg ttc tta Arg Leu Leu Gly Ala Ala Val Ala Thr Ala Glu Thr Leu Thr Phe Leu 265 270 275	1050
gat gct cac tgt gag tgc ttc tat ggc tgg ctg gaa cct ctg ctg gcc Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu Pro Leu Leu Ala 280 285 290	1098
agg ata gct gag aac tac act gcc gtg gtg agt cca gac atc gca tcc Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro Asp Ile Ala Ser 295 300 305	1146
ata gat cta aac aca ttt gaa ttc aac aag cct tct ccg tac gga agc Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser Pro Tyr Gly Ser 310 315 320	1194

aac cat aac cgt gga aat ttt gac tgg agc ctt tcc ttt ggc tgg gag Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser Phe Gly Trp Glu 325 330 335 340	1242
tca ctt cct gat cat gag aag caa aga agg aaa gat gaa acc tac cca Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp Glu Thr Tyr Pro 345 350 355	1290
att aag acc ccc acc ttt gca gga ggc ctt ttt tct ata tct aaa aaa Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser Ile Ser Lys Lys 360 365 370	1338
tat ttt gag cac att gga agt tac gat gaa gaa atg gaa atc tgg gga Tyr Phe Glu His Ile Gly Ser Tyr Asp Glu Glu Met Glu Ile Trp Gly 375 380 385	1386
ggg gaa aat ata gaa atg tca ttc cga gtg tgg caa tgt ggt ggg cag Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln Cys Gly Gly Gln 390 395 400	1434
ttg gag att atg cct tgc tct gtt gga cat gtt ttt cgc agc aaa Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val Phe Arg Ser Lys 405 410 415 420	1482
agc cct cat acc ttc cca aaa ggc acg cag gtg att gct cgt aac caa Ser Pro His Thr Phe Pro Lys Gly Thr Gln Val Ile Ala Arg Asn Gln 425 430 435	1530
gtt cgc ctt gca gag gtc tgg atg gac gaa tac aag gaa ata ttt tat Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys Glu Ile Phe Tyr 440 445 450	1578
agg aga aac aca gat gca gca aaa atc gtt aag caa aaa tca ttt ggt Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln Lys Ser Phe Gly 455 460 465	1626
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ttt acc tgg tac ctg aac act att tac ccg gaa ggc tat gtg cca gac Phe Thr Trp Tyr Leu Asn Thr Ile Tyr Pro Glu Ala Tyr Val Pro Asp 485 490 495 500	1722
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tac acg tgc cac ggc ctc ggg gga aat cag tac ttc gag tat tct gct Tyr Thr Cys His Gly Leu Gly Asn Gln Tyr Phe Glu Tyr Ser Ala 535 540 545	1866
cag cgt gaa atc cgg cac aac atc cag aag gag ctg tgt ctt cat gct Gln Arg Glu Ile Arg His Asn Ile Gln Lys Glu Leu Cys Leu His Ala 550 555 560	1914

act cag ggt gtc gtc cag ctg aag gca tgt gtc tat aaa ggt cac agg		1962
Thr Gln Gly Val Val Gln Leu Lys Ala Cys Val Tyr Lys Gly His Arg		
565	570	575
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acc atc gcc cct gga gaa cag ata tgg gag att cggtt gac caa ctt		2010
Thr Ile Ala Pro Gly Glu Gln Ile Trp Glu Ile Arg Lys Asp Gln Leu		
585	590	595
cta tat aat cca tta ttt aaa atg tgc ctt tca tca aat gga gag cat		2058
Leu Tyr Asn Pro Leu Phe Lys Met Cys Leu Ser Ser Asn Gly Glu His		
600	605	610
cca aac tta gtg cca tgt gac gca aca gat cta ctc caa aaa tgg att		2106
Pro Asn Leu Val Pro Cys Asp Ala Thr Asp Leu Leu Gln Lys Trp Ile		
615	620	625
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Phe Ser Gln Asn Glu		
630		
acatactctt cctcataaaaa ctgtgactag gcatacactg tagttgtga aaattatgca		2214
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His Arg Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Leu Val

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30

Val Leu Ile Leu Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
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Glu Ser Lys Met Glu Arg Asn Leu Lys Asn Lys Met Leu Asp
 50 55 60

Phe Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
 65 70 75 80

Gln Ile Gly Ala Pro Ile Lys Glu Asn Ile Asp Val Arg Glu Arg Pro
 85 90 95

Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Phe Asp
 100 105 110

Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Pro Phe
 115 120 125

Lys Ile Thr His Leu Ser Pro Glu Glu Gln Lys Glu Lys Glu Arg Gly
 130 135 140

Glu Thr Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
 145 150 155 160

His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
 165 170 175

Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
 180 185 190

Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val
 195 200 205

Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp
 210 215 220

Asp Ala Ser Val Asp Asp Tyr Leu His Glu Lys Leu Glu Glu Tyr Ile
 225 230 235 240

Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Gln Glu Arg Lys Gly
 245 250 255

Leu Ile Thr Ala Arg Leu Leu Gly Ala Ala Val Ala Thr Ala Glu Thr

260

265

270

Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu
275 280 285

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290 295 300

Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser
305 310 315 320

Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser
325 330 335

Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp
340 345 350

Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser
355 360 365

Ile Ser Lys Lys Tyr Phe Glu His Ile Gly Ser Tyr Asp Glu Glu Met
370 375 380

Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln
385 390 395 400

Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val
405 410 415

Phe Arg Ser Lys Ser Pro His Thr Phe Pro Lys Gly Thr Gln Val Ile
420 425 430

Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys
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Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln
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Lys Ser Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys Lys Arg Leu
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Gln Cys Lys Asn Phe Thr Trp Tyr Leu Asn Thr Ile Tyr Pro Glu Ala
485 490 495

Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val

500

505

510

Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys
515 520 525

Pro Leu Ile Leu Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe
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Glu Tyr Ser Ala Gln Arg Glu Ile Arg His Asn Ile Gln Lys Glu Leu
545 550 555 560

Cys Leu His Ala Thr Gln Gly Val Val Gln Leu Lys Ala Cys Val Tyr
565 570 575

Lys Gly His Arg Thr Ile Ala Pro Gly Glu Gln Ile Trp Glu Ile Arg
580 585 590

Lys Asp Gln Leu Leu Tyr Asn Pro Leu Phe Lys Met Cys Leu Ser Ser
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Asn Gly Glu His Pro Asn Leu Val Pro Cys Asp Ala Thr Asp Leu Leu
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Gln Lys Trp Ile Phe Ser Gln Asn Glu
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ctgctctccc cgggctgcgg gcc atg gcc acg gcg gag cgg aga gcc ctc ggc 173
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly
1 5 10
atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221
Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
15 20 25
ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269
Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly

30

35

40

ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His 45	50	55	317
tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile 60	65	70	365
agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr 75	80	85	413
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu 95	100	105	461
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu 110	115	120	509
gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly 125	130	135	557
tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His 140	145	150	605
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp 155	160	165	653
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr 175	180	185	701
cag ctg gcc cg att gcg gac agt aag gat cat gtg ttt ccc gtg aat Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn 190	195	200	749
gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys 205	210	215	797
tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly 220	225	230	845
gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg 235	240	245	893
aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr 255	260	265	941
ctc aat gag aag ccc ttt tct gtg gaa gat act tat tta ctg tgt cca Leu Asn Glu Lys Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro			989

270	275	280	
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atg aac gat ggc ctc tct ttt atc tcc agt tct gtc atc atc acc acc Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr Thr 300	305	310	1085
aca cac tgt tct gac ggt tcc atc ctg gcc atc gcc ctg ctg atc ctg Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu 315	320	325	1133
ttc ctg ctc cta gcc ctg gct ctc tgg tgg ttc tgg ccc ctc tgc Phe Leu Leu Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys 335	340	345	1181
tgc act gtg att atc aag gag gtc cct cca ccc cct gcc gag gag agt Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Pro Ala Glu Glu Ser 350	355	360	1229
gag gaa gaa gat gat gat ggt ctg cct aag aaa aag tgg cca acg gta Glu Glu Asp Asp Asp Gly Leu Pro Lys Lys Trp Pro Thr Val 365	370	375	1277
gac gcc tct tat tat ggt ggg aga ggc gtt gga ggc att aaa aga atg Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Ile Lys Arg Met 380	385	390	1325
gag gtt cgt tgg gga gaa aag ggc tcc aca gaa gaa ggt gct aag ttg Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu 395	400	405	1373
gaa aag gca aag aat gca aga gtc aag atg ccg gag cag gaa tat gaa Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu Gln Glu Tyr Glu 415	420	425	1421
ttc cct gag ccg cga aat ctc aac aac aat atg cgt cgg cct tct tcc Phe Pro Glu Pro Arg Asn Leu Asn Asn Asn Met Arg Arg Pro Ser Ser 430	435	440	1469
ccc cgg aag tgg tac tct cca atc aag gga aaa ctc gat gcc ttg tgg Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp 445	450	455	1517
gtc cta ctg agg aaa gga tat gat cgt gtg tct gtg atg cgt cca cag Val Leu Leu Arg Lys Gly Tyr Asp Arg Val Ser Val Met Arg Pro Gln 460	465	470	1565
cca gga gac acg ggg cgc tgc atc aac ttc acc agg gtc aag aac aac Pro Gly Asp Thr Gly Arg Cys Ile Asn Phe Thr Arg Val Lys Asn Asn 475	480	485	1613
cag cca gcc aag tac cca ctc aac aac gcc tac cac acc tcc tcg ccg Gln Pro Ala Lys Tyr Pro Leu Asn Asn Ala Tyr His Thr Ser Ser Pro 495	500	505	1661
cct cct gcc ccc atc tac act ccc cca cct cct gcg ccc cac tgc cct Pro Pro Ala Pro Ile Tyr Thr Pro Pro Pro Ala Pro His Cys Pro			1709

510	515	520	
ccc ccg ccc ccc agc gcc cct acc ccc atc ccg tcc cca cct tcc Pro Pro Pro Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser	525	530	1757
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acc ctt ccc cct ccc cag gct cca cct ccc aac agg gca cct cct Thr Leu Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro	540	545	1805
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ccc tcc cgc cct ccc cca agg cct tct gtc tag agcccaaagt tcctgctctg Pro Ser Arg Pro Pro Arg Pro Ser Val	555	560	1858
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<400> 28

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Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
35 40 45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
50 55 60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
115 120 125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
130 135 140

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145 150 155 160

Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
165 170 175

Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
180 185 190

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
195 200 205

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
210 215 220

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225 230 235 240

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
245 250 255

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
260 265 270

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
275 280 285

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
290 295 300

Phe Ile Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305 310 315 320

Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
325 330 335

Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
340 345 350

Glu Val Pro Pro Pro Ala Glu Glu Ser Glu Glu Asp Asp Asp
355 360 365

Gly Leu Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly
370 375 380

Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
385 390 395 400

Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
405 410 415

Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
420 425 430

Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
435 440 445

Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
450 455 460

Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465 470 475 480

Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
485 490 495

Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
500 505 510

Thr Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala
515 520 525

Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro
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Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro
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Arg Pro Ser Val

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<221> CDS
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aggctcaaag	ctggctctgc	aggggac	atg aga ggc aca ccg aag acc cac ctc	Met Arg Gly Thr Pro Lys Thr His Leu		174
			1	5		
ctg gcc ttc tcc ctc ctc tgc ctc ctc tca	aag gtg cgt acc cag ctg					222
Leu Ala Phe Ser Leu Leu Cys Leu Ser Lys Val Arg Thr Gln Leu						
10	15	20	25			
tgc ccg aca cca tgt acc tgc ccc tgg cca cct ccc cga tgc ccg ctg						270
Cys Pro Thr Pro Cys Thr Cys Pro Trp Pro Pro Arg Cys Pro Leu						
30	35	40				
gga gta ccc ctg gtg ctg gat ggc tgt ggc tgc tgc cgg gta tgt gca						318
Gly Val Pro Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala						
45	50	55				
cgg cgg ctg ggg gag ccc tgc gac caa ctc cac gtc tgc gac gcc agc						366
Arg Arg Leu Gly Glu Pro Cys Asp Gln Leu His Val Cys Asp Ala Ser						
60	65	70				
cag ggc ctg gtc tgc cag ccc ggg gca gga ccc ggt ggc cgg ggg gcc						414
Gln Gly Leu Val Cys Gln Pro Gly Ala Gly Pro Gly Arg Gly Ala						
75	80	85				
ctg tgc ctc ttg gca gag gac agc agc tgt gag gtg aac ggc cgc						462
Leu Cys Leu Leu Ala Glu Asp Asp Ser Ser Cys Glu Val Asn Gly Arg						
90	95	100	105			
ctg tat cgg gaa ggg gag acc ttc cag ccc cac tgc agc atc cgc tgc						510
Leu Tyr Arg Glu Gly Glu Thr Phe Gln Pro His Cys Ser Ile Arg Cys						
110	115	120				
cgc tgc gag gac ggc ggc ttc acc tgc gtg ccg ctg tgc agc gag gat						558
Arg Cys Glu Asp Gly Gly Phe Thr Cys Val Pro Leu Cys Ser Glu Asp						
125	130	135				
gtg cgg ctg ccc agc tgg gac tgc ccc cac ccc agg agg gtc gag gtc						606
Val Arg Leu Pro Ser Trp Asp Cys Pro His Pro Arg Arg Val Glu Val						
140	145	150				
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Leu Gly Lys Cys Cys Pro Glu Trp Val Cys Gly Gln Gly Gly Leu						
155	160	165				
ggg acc cag ccc ctt cca gcc caa gga ccc cag ttt tct ggc ctt gtc						702
Gly Thr Gln Pro Leu Pro Ala Gln Gly Pro Gln Phe Ser Gly Leu Val						
170	175	180	185			
tct tcc ctg ccc cct ggt gtc ccc tgc cca gaa tgg agc acg gcc tgg						750
Ser Ser Leu Pro Pro Gly Val Pro Cys Pro Glu Trp Ser Thr Ala Trp						
190	195	200				
gga ccc tgc tcg acc acc tgt ggg ctg ggc atg gcc acc cgg gtg tcc						798
Gly Pro Cys Ser Thr Thr Cys Gly Leu Gly Met Ala Thr Arg Val Ser						
205	210	215				

aac cag aac cgc ttc tgc cga ctg gag acc cag cgc cgc ctg tgc ctg		846
Asn Gln Asn Arg Phe Cys Arg Leu Glu Thr Gln Arg Arg Leu Cys Leu		
220	225	230
tcc agg ccc tgc cca ccc tcc agg ggt cgc agt cca caa aac aac agt gcc		894
Ser Arg Pro Cys Pro Pro Ser Arg Gly Arg Ser Pro Gln Asn Ser Ala		
235	240	245
ttc tag agccgggctg ggaatgggaa cacgggtgtcc accatccccca gctgggtggcc		950
Phe		
250		
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<400> 30

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Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val Leu Asp		
35	40	45

Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Pro Cys		
50	55	60

Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys Gln Pro			
65	70	75	80

Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala Glu Asp

85

90

95

Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly Glu Thr
100 105 110

Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly Gly Phe
115 120 125

Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
130 135 140

Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys Pro Glu
145 150 155 160

Trp Val Cys Gly Gln Gly Gly Leu Gly Thr Gln Pro Leu Pro Ala
165 170 175

Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro Gly Val
180 185 190

Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr Cys
195 200 205

Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys Arg
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Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe
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Ala Asp Ala Gly Ile Arg Arg Val Val Pro Ser Asp Leu Tyr Pro Leu

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tcc gcc aaa gcg aca gga gct aca cag cag gat gcc aat gcc tct tcc Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser Ser 35	40	45	201
ctc tta gac atc tat agc ttc tgg ctc aag tct gcc aag gtc cca gag Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Ala Lys Val Pro Glu 50	55	60	249
cga aag tta cag gca aat gga cca gtg gct aag aaa gct aag aag aag Arg Lys Leu Gln Ala Asn Gly Pro Val Ala Lys Lys Ala Lys Lys Lys 70	75	80	297
gcc tca tcc agt gac agt gag gac agc gag gag gag gag gaa gtt Ala Ser Ser Ser Asp Ser Glu Asp Ser Ser Glu Glu Glu Glu Glu Val 85	90	95	345
caa ggg cct cca gca aag aag gct gct gta cct gcc aag cga gtc ggt Gln Gly Pro Pro Ala Lys Lys Ala Ala Val Pro Ala Lys Arg Val Gly 100	105	110	393
ctg cct cgg aag gct gca gcc aaa gca tca gag agt agc agc agt Leu Pro Pro Gly Lys Ala Ala Lys Ala Ser Glu Ser Ser Ser Ser 115	120	125	441
gaa gag tcc aga gat gat gat gag gag gac caa aag aaa cag cct Glu Glu Ser Arg Asp Asp Asp Glu Glu Asp Gln Lys Lys Gln Pro 130	135	140	489
gtc cag aag gga gtt aag ccc caa gca aag gca gcc aaa gct cct cct Val Gln Lys Gly Val Lys Pro Gln Ala Lys Ala Ala Lys Ala Pro Pro 150	155	160	537
aag aag gcc aag agc tct gat tct gat tct gac tca agc tcc gag gat Lys Lys Ala Lys Ser Ser Asp Ser Asp Ser Ser Ser Glu Asp 165	170	175	585
gag cca cca aag aac cag aag cca aag ata aca cct gtg aca gtt aaa Glu Pro Pro Lys Asn Gln Lys Pro Lys Ile Thr Pro Val Thr Val Lys 180	185	190	633
gct cag act aaa gcc cct ccc aaa cca gct cga gca gca cct aaa ata Ala Gln Thr Lys Ala Pro Pro Lys Pro Ala Arg Ala Ala Pro Lys Ile 195	200	205	681
gcc aat ggt aaa gca gcc agt agc agc agt agc agc agc agc agt Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser 210	215	220	729
agc agt gat gac tca gag gag aag gca gca gcc acc ccc aag aag Ser Ser Asp Asp Ser Glu Glu Lys Ala Ala Ala Thr Pro Lys Lys 230	235	240	777
act gta cct aaa aag caa gtt gtg gcc aaa gcc cca gtg aaa gca gct Thr Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Ala Ala			825

245	250	255	
acc acc cct acc cg ^g aag agt tct agc agt gag gat tcc tcc agt gac Thr Thr Pro Thr Arg Lys Ser Ser Ser Glu Asp Ser Ser Ser Asp	260	265	873
	270		
gag gaa gag gag caa aaa aaa ccc atg aaa aat aaa cca ggt ccc tac Glu Glu Glu Glu Gln Lys Lys Pro Met Lys Asn Lys Pro Gly Pro Tyr	275	280	921
	285		
agt tac gcc ccc ccg cct tct gct ccc cca cca aag aag tct ctg gga Ser Tyr Ala Pro Pro Ser Ala Pro Pro Pro Lys Lys Ser Leu Gly	290	295	969
	300	305	
acc cag cct ccc aag aag gct gtg gag aag cag cag cct gtg gaa agc Thr Gln Pro Pro Lys Lys Ala Val Glu Lys Gln Gln Pro Val Glu Ser	310	315	1017
	320		
agt gaa gac agc agt gat gag tct gat tca agt tct gaa gaa gag aag Ser Glu Asp Ser Ser Asp Glu Ser Asp Ser Ser Glu Glu Glu Lys	325	330	1065
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aaa ccc cca act aag gca gta gtc tct aaa gca acc act aaa cca cct Lys Pro Pro Thr Lys Ala Val Val Ser Lys Ala Thr Thr Lys Pro Pro	340	345	1113
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	380	385	
aat tct tca aat aag cca gct gtc acc acc aag tca cct gca gtg aag Asn Ser Ser Asn Lys Pro Ala Val Thr Thr Lys Ser Pro Ala Val Lys	390	395	1257
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cca gct gca gcc ccc aag caa cct gtg ggc ggt ggc cag aag ctt ctg Pro Ala Ala Ala Pro Lys Gln Pro Val Gly Gly Gln Lys Leu Leu	405	410	1305
	415		
acg aga aag gct gac agc agc tcc agc gag gaa gag agc agc tcc agt Thr Arg Lys Ala Asp Ser Ser Ser Glu Glu Glu Ser Ser Ser Ser	420	425	1353
	430		
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	445		
act gcc aaa gca gct cta tct ctg cct gcc aag cag gct cct cag ggt Thr Ala Lys Ala Ala Leu Ser Leu Pro Ala Lys Gln Ala Pro Gln Gly	450	455	1449
	460	465	
agt agg gac agc agc tct gat tca gac agc tcc agc agt gag gag gag Ser Arg Asp Ser Ser Asp Ser Asp Ser Ser Ser Glu Glu Glu Glu	470	475	1497
	480		
gaa gag aag aca tct aag tct gca gtt aag aag aag cca cag aag gta Glu Glu Lys Thr Ser Ser Ala Val Lys Lys Pro Gln Lys Val			1545

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gaa gag aag ctc aag ggc aag ggc tct cca aga cca caa gcc ccc aag Glu Glu Lys Leu Lys Gly Lys Ser Pro Arg Pro Gln Ala Pro Lys 530	535	540	1689
gcc aat ggc acc tct gca ctg act gcc cag aat gga aaa gca gct aag Ala Asn Gly Thr Ser Ala Leu Thr Ala Gln Asn Gly Lys Ala Ala Lys 550	555	560	1737
aac agt gag gag gag gaa gaa aag aag aag gcg gca gtg gta gtt Asn Ser Glu Glu Glu Glu Lys Lys Lys Ala Ala Val Val Val 565	570	575	1785
tcc aaa tca ggt tca tta aag aag cgg aag cag aat gag gct gcc aag Ser Lys Ser Gly Ser Leu Lys Lys Arg Lys Gln Asn Glu Ala Ala Lys 580	585	590	1833
gag gca gag act cct cag gcc aag aag ata aag ctt cag acc cct aac Glu Ala Glu Thr Pro Gln Ala Lys Lys Ile Lys Leu Gln Thr Pro Asn 595	600	605	1881
aca ttt cca aaa agg aag aaa gga gaa aaa agg gca tca tcc cca ttc Thr Phe Pro Lys Arg Lys Lys Gly Glu Lys Arg Ala Ser Ser Pro Phe 610	615	620	1929
cga agg gtc agg gag gag gaa att gag gtg gat tca cga gtt gcg gac Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val Ala Asp 630	635	640	1977
aac tcc ttt gat gcc aag cga ggt gca gcc gga gac tgg gga gag cga Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly Glu Arg 645	650	655	2025
gcc aat cag gtt ttg aag ttc acc aaa ggc aag tcc ttt cgg cat gag Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg His Glu 660	665	670	2073
aaa acc aag aag aag cgg ggc agc tac cgg gga ggc tca atc tct gtc Lys Thr Lys Lys Arg Gly Ser Tyr Arg Gly Gly Ser Ile Ser Val 675	680	685	2121
cag gtc aat tct att aag ttt gac agc gag tga cctgaggcca tcttcggta Gln Val Asn Ser Ile Lys Phe Asp Ser Glu 690	695		2174
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Ser Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Ala Lys Val Pro
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Glu Arg Lys Leu Gln Ala Asn Gly Pro Val Ala Lys Lys Ala Lys Lys
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Val Gln Gly Pro Pro Ala Lys Lys Ala Ala Val Pro Ala Lys Arg Val
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Gly Leu Pro Pro Gly Lys Ala Ala Lys Ala Ser Glu Ser Ser Ser
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Ser Glu Glu Ser Arg Asp Asp Asp Asp Glu Glu Asp Gln Lys Lys Gln
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Pro Val Gln Lys Gly Val Lys Pro Gln Ala Lys Ala Ala Lys Ala Pro
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Pro Lys Lys Ala Lys Ser Ser Asp Ser Asp Ser Asp Ser Ser Ser Glu
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Asp Glu Pro Pro Lys Asn Gln Lys Pro Lys Ile Thr Pro Val Thr Val
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Lys Ala Gln Thr Lys Ala Pro Pro Lys Pro Ala Arg Ala Ala Pro Lys
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Ile Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser
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Ser Ser Ser Asp Asp Ser Glu Glu Glu Lys Ala Ala Ala Thr Pro Lys
225 230 235 240

Lys Thr Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Ala
245 250 255

Ala Thr Thr Pro Thr Arg Lys Ser Ser Ser Ser Glu Asp Ser Ser Ser
260 265 270

Asp Glu Glu Glu Glu Gln Lys Lys Pro Met Lys Asn Lys Pro Gly Pro
275 280 285

Tyr Ser Tyr Ala Pro Pro Ser Ala Pro Pro Pro Lys Lys Ser Leu
290 295 300

Gly Thr Gln Pro Pro Lys Lys Ala Val Glu Lys Gln Gln Pro Val Glu
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Ser Ser Glu Asp Ser Ser Asp Glu Ser Asp Ser Ser Ser Glu Glu Glu
325 330 335

Lys Lys Pro Pro Thr Lys Ala Val Val Ser Lys Ala Thr Thr Lys Pro
340 345 350

Pro Pro Ala Lys Lys Ala Ala Glu Ser Ser Ser Asp Ser Ser Asp Ser
355 360 365

Asp Ser Ser Glu Asp Asp Glu Ala Pro Ser Lys Pro Ala Gly Thr Thr
370 375 380

Lys Asn Ser Ser Asn Lys Pro Ala Val Thr Thr Lys Ser Pro Ala Val
385 390 395 400

Lys Pro Ala Ala Ala Pro Lys Gln Pro Val Gly Gly Gly Gln Lys Leu
405 410 415

Leu Thr Arg Lys Ala Asp Ser Ser Ser Ser Glu Glu Glu Ser Ser Ser
420 425 430

Ser Glu Glu Glu Lys Thr Lys Lys Met Val Ala Thr Thr Lys Pro Lys
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Ala Thr Ala Lys Ala Ala Leu Ser Leu Pro Ala Lys Gln Ala Pro Gln
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Gly Ser Arg Asp Ser Ser Ser Asp Ser Asp Ser Ser Ser Glu Glu
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Glu Glu Glu Lys Thr Ser Lys Ser Ala Val Lys Lys Lys Pro Gln Lys
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Val Ala Gly Gly Ala Ala Pro Ser Lys Pro Ala Ser Ala Lys Lys Gly
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Lys Ala Glu Ser Ser Asn Ser Ser Ser Asp Asp Ser Ser Glu Glu
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Lys Ala Asn Gly Thr Ser Ala Leu Thr Ala Gln Asn Gly Lys Ala Ala
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Lys Asn Ser Glu Glu Glu Glu Lys Lys Lys Ala Ala Val Val
565 570 575

Val Ser Lys Ser Gly Ser Leu Lys Lys Arg Lys Gln Asn Glu Ala Ala
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Lys Glu Ala Glu Thr Pro Gln Ala Lys Lys Ile Lys Leu Gln Thr Pro
595 600 605

Asn Thr Phe Pro Lys Arg Lys Lys Gly Glu Lys Arg Ala Ser Ser Pro
610 615 620

Phe Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val Ala
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Asp Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly Glu
645 650 655

Arg Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg His
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	tat ggc cta ttg aag cac agt cg c gac ttc ttg gac ttc ttc tgg gac Tyr Gly Leu Leu Lys His Ser Arg Glu Phe Leu Asp Phe Phe Trp Asp 30 35 40	148
	att gcg aag cct gag cag gag acg cga ctt gcg gcc acg gag aag ctg Ile Ala Lys Pro Glu Gln Glu Thr Arg Leu Ala Ala Thr Glu Lys Leu 45 50 55	196
	ctg gag tat ctg cgt ggc agg ccg aag ggg tcc gag atg aaa tat gcc Leu Glu Tyr Leu Arg Gly Arg Pro Lys Gly Ser Glu Met Lys Tyr Ala 60 65 70	244
	ctg aag cgt cta atc acg gga ctc ggg gtc ggg cga gaa aca gcc cg Leu Lys Arg Leu Ile Thr Gly Leu Gly Val Gly Arg Glu Thr Ala Arg 75 80 85	292
	ccc tgc tac agt ttg gcc ctg gca cag ctg tta cag tct ttt gaa gac Pro Cys Tyr Ser Leu Ala Leu Ala Gln Leu Leu Gln Ser Phe Glu Asp 90 95 100 105	340
	ctc ccc ttg tgc agc atc ctg cag cag ata caa gaa aaa tat gac ctg Leu Pro Leu Cys Ser Ile Leu Gln Gln Ile Gln Glu Lys Tyr Asp Leu 110 115 120	388
	cat cag gtg aag aag gca atg ctg aga cct gct ctc ttt gca aac ctg His Gln Val Lys Lys Ala Met Leu Arg Pro Ala Leu Phe Ala Asn Leu 125 130 135	436
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gag gca ctg atg aag tcg gtg aag ctg ctg cag gcc ctg gcc cag tac Glu Ala Leu Met Lys Ser Val Lys Leu Leu Gln Ala Leu Ala Gln Tyr 155	160	165	532
caa aac cac ttg cag gag cag ccc cgg aag gcc ctg gtg gac atc ctc Gln Asn His Leu Gln Glu Gln Pro Arg Lys Ala Leu Val Asp Ile Leu 170	175	180	185
tcc gag gtc tcg aag gcc aca ttg cag gag atc ctg ccg gag gtc ctc Ser Glu Val Ser Lys Ala Thr Leu Gln Glu Ile Leu Pro Glu Val Leu 190	195	200	628
aaa gcc gac ttg aat ata ata ctc agc tcc cct gaa cag cta gag ctc Lys Ala Asp Leu Asn Ile Ile Leu Ser Ser Pro Glu Gln Leu Glu Leu 205	210	215	676
ttc ctc ctg gcc cag cag aag gtg ccc tcc aag ctc aag aag ctg gtg Phe Leu Leu Ala Gln Gln Lys Val Pro Ser Lys Leu Lys Lys Leu Val 220	225	230	724
gga tcc gtg aac cta ttc tca gat gag aat gtc ccc agg ctg gtg aat Gly Ser Val Asn Leu Phe Ser Asp Glu Asn Val Pro Arg Leu Val Asn 235	240	245	772
gtg ctg aag atg gcc gcc tcc tct gtg aag aag gac cgc aag ctg ccc Val Leu Lys Met Ala Ala Ser Ser Val Lys Lys Asp Arg Lys Leu Pro 250	255	260	265
gcc att gct ctg gac ctg ctc cgc ctg gcg ctc aag gaa gac aag ttc Ala Ile Ala Leu Asp Leu Leu Arg Leu Ala Leu Lys Glu Asp Lys Phe 270	275	280	868
cca cgg ttc tgg aag gag gtg gtg gaa caa ggg ctg ctg aag atg cag Pro Arg Phe Trp Lys Glu Val Val Glu Gln Gly Leu Leu Lys Met Gln 285	290	295	916
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Leu Arg Ala Met Phe Leu Gln Pro Asp Leu Asp Ser Leu Val Asp Phe	
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Ser Thr Asn Asn Gln Lys Lys Ala Gln Asp Ser Ser Leu His Met Pro	
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Glu Arg Ala Val Phe Arg Leu Arg Lys Trp Ile Ile Phe Arg Leu Val	
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Ser Ile Val Asp Ser Leu His Leu Glu Met Glu Glu Ala Leu Thr Glu	
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Gln Val Ala Arg Phe Cys Leu Phe His Ser Phe Phe Val Thr Lys Lys	
475 480 485	
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Pro Thr Ser Gln Ile Pro Glu Thr Lys His Pro Phe Ser Phe Pro Leu	
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Gln Thr Leu Ser Thr Gln Phe Lys Gln Ala Pro Gly Gln Thr Gln Gly	
525 530 535	
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Gly Gln Pro Trp Thr Tyr His Leu Val Gln Phe Ala Asp Leu Leu Leu	
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Asn His Ser His Asn Val Thr Thr Val Thr Pro Phe Thr Ala Gln Gln	
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His Gln Ala Trp Asp Arg Met Leu Gln Thr Leu Lys Glu Leu Glu Ala	
570 575 580 585	
cac tcc gca gag gcc agg gct gct gcc ttc cag cac ctt ctg ctc ttg	1828
His Ser Ala Glu Ala Arg Ala Ala Phe Gln His Leu Leu Leu Phe	
590 595 600	
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Val Gly Ile His Leu Leu Lys Ser Pro Ala Glu Ser Cys Asp Leu Leu	
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Gly Asp Ile Gln Thr Cys Ile Arg Lys Ser Leu Gly Glu Lys Pro Arg	
620 625 630	

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Arg Ser Arg Thr Lys Thr Ile Asp Pro Gln Glu Pro Pro Trp Val Glu	
635 640 645	
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Val Leu Val Glu Ile Leu Ala Leu Leu Ala Gln Pro Ser His Leu	
650 655 660 665	
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Met Arg Gln Val Ala Arg Ser Val Phe Gly His Ile Cys Ser His Leu	
670 675 680	
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Thr Pro Arg Ala Leu Gln Leu Ile Leu Asp Val Leu Asn Pro Glu Thr	
685 690 695	
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Ser Glu Asp Glu Asn Asp Arg Val Val Val Thr Asp Asp Ser Asp Glu	
700 705 710	
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Arg Arg Leu Lys Gly Ala Glu Asp Lys Ser Glu Glu Gly Glu Asp Asn	
715 720 725	
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810 815 820 825	
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Val Leu Leu Gly	Val Leu Gln Gly Gln	Gln Gln Ser Leu Gln	Gln	
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Gly Ala His Ser	Thr Gly Ser Ser Arg	Leu His Asp Leu Tyr	Trp	
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Gln Ala Met Lys	Thr Leu Gly Val Gln	Arg Pro Lys Leu Glu	Lys	
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Lys Asp Ala Lys	Glu Ile Pro Ser Ala	Thr Gln Ser Pro Ile	Ser	
1155	1160	1165		
aag aag cgg aag	aaa aag gga ttc ttg	cca gag acg aag aag	cgc	3568
Lys Lys Arg Lys	Lys Lys Gly Phe Leu	Pro Glu Thr Lys Lys	Arg	
1170	1175	1180		
aag aaa cgc aag	tca gag gat ggc acg	cca gcg gag gat ggc	aca	3613
Lys Lys Arg Lys	Ser Glu Asp Gly Thr	Pro Ala Glu Asp Gly	Thr	
1185	1190	1195		
cct gca gcc acc	ggc ggg agc cag ccc	ccc agc atg ggc agg	aag	3658
Pro Ala Ala Thr	Gly Gly Ser Gln Pro	Pro Ser Met Gly Arg	Lys	
1200	1205	1210		
aag agg aac agg	aca aag gct aag gtc	cca gcc cag gca aac	ggg	3703
Lys Arg Asn Arg	Thr Lys Ala Lys Val	Pro Ala Gln Ala Asn	Gly	
1215	1220	1225		
acg cca acc acc	aag agt cca gcc cct	ggc gcc ccc acc cgg	agc	3748
Thr Pro Thr Thr	Lys Ser Pro Ala Pro	Gly Ala Pro Thr Arg	Ser	
1230	1235	1240		
ccc agc acc cct	gcc aaa tcc cca aaa	ctg cag aag aaa aac	cag	3793
Pro Ser Thr Pro	Ala Lys Ser Pro Lys	Leu Gln Lys Lys Asn	Gln	
1245	1250	1255		
aag ccg tcc cag	gtg aat gga gct ccc	ggg tcc ccc acg gaa	cct	3838
Lys Pro Ser Gln	Val Asn Gly Ala Pro	Gly Ser Pro Thr Glu	Pro	
1260	1265	1270		
gca ggc caa aag	cag cat cag aag gct	ctt ccc aaa aag ggg	gtc	3883
Ala Gly Gln Lys	Gln His Gln Lys Ala	Leu Pro Lys Lys Gly	Val	
1275	1280	1285		
ttg ggc aaa tca	cca ctg tcc gcg ctg	gca cgg aaa aag gca	agg	3928
Leu Gly Lys Ser	Pro Leu Ser Ala Leu	Ala Arg Lys Lys Ala	Arg	
1290	1295	1300		
ctg tct ttg gtc	atc agg agt ccc agc	ctg ctt cag agt ggg	gcc	3973
Leu Ser Leu Val	Ile Arg Ser Pro Ser	Leu Leu Gln Ser Gly	Ala	
1305	1310	1315		
aag aag aaa gca	cag gtg agg aag gca	ggg aag ccc tga gcacaggtac		4022
Lys Lys Lys Ala	Gln Val Arg Lys Ala	Gly Lys Pro		
1320	1325			

gggccccct cagccctgc ctccatctgc ctgagacgcc tattttttt tttttaaaac	4082
catgattta atacgcaagc tgtttctaag gcgctgccac tggggagggt ggctgtgcc	4142
gcctgcccgg gcatecctgct ctggcaagca cagcctgagc cattcctgct ggggtcccag	4202
ggtcagaga cctccccacc cccagttctg ggctgggatc ctggctccag ggccatgtcc	4262
agggctctgg tggttgctg ggttggtgca tggtgatgtg ctggctgcag gcaggtgtga	4322
ccatctctcg tgcctgccac ctcttgccc ccaggcttt ttgctgtgag ggagccacca	4382
gggggtgatt taaataggtt tatttcttca tttacaagag gaatatattt ggcttctctc	4442
ttaagactct gagattcaca atcagcagct ctaaaaaata aaggagcagt ttggcttccg	4502
gaaggaagag gaggctaaaa aaaaaaaaaa aaaaaa	4538

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Met Glu Ser Arg Asp Pro Ala Gln Pro Met Ser Pro Gly Glu Ala Thr
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Gln Ser Gly Ala Arg Pro Ala Asp Arg Tyr Gly Leu Leu Lys His Ser
 20 25 30

Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Glu Gln Glu
 35 40 45

Thr Arg Leu Ala Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg Gly Arg
 50 55 60

Pro Lys Gly Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly
 65 70 75 80

Leu Gly Val Gly Arg Glu Thr Ala Arg Pro Cys Tyr Ser Leu Ala Leu
 85 90 95

Ala Gln Leu Leu Gln Ser Phe Glu Asp Leu Pro Leu Cys Ser Ile Leu
 100 105 110

Gln Gln Ile Gln Glu Lys Tyr Asp Leu His Gln Val Lys Lys Ala Met
 115 120 125

Leu Arg Pro Ala Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe

130

135

140

Gln Ser Gly Arg Leu Val Lys Asp Gln Glu Ala Leu Met Lys Ser Val
145 150 155 160

Lys Leu Leu Gln Ala Leu Ala Gln Tyr Gln Asn His Leu Gln Glu Gln
165 170 175

Pro Arg Lys Ala Leu Val Asp Ile Leu Ser Glu Val Ser Lys Ala Thr
180 185 190

Leu Gln Glu Ile Leu Pro Glu Val Leu Lys Ala Asp Leu Asn Ile Ile
195 200 205

Leu Ser Ser Pro Glu Gln Leu Glu Leu Phe Leu Ala Gln Gln Lys
210 215 220

Val Pro Ser Lys Leu Lys Lys Leu Val Gly Ser Val Asn Leu Phe Ser
225 230 235 240

Asp Glu Asn Val Pro Arg Leu Val Asn Val Leu Lys Met Ala Ala Ser
245 250 255

Ser Val Lys Lys Asp Arg Lys Leu Pro Ala Ile Ala Leu Asp Leu Leu
260 265 270

Arg Leu Ala Leu Lys Glu Asp Lys Phe Pro Arg Phe Trp Lys Glu Val
275 280 285

Val Glu Gln Gly Leu Leu Lys Met Gln Phe Trp Pro Ala Ser Tyr Leu
290 295 300

Cys Phe His Leu Leu Gly Ala Ala Leu Pro Leu Leu Thr Lys Glu Gln
305 310 315 320

Leu His Leu Val Met Gln Gly Asp Val Ile Arg His Tyr Gly Glu His
325 330 335

Val Cys Thr Ala Lys Leu Pro Lys Gln Phe Lys Phe Ala Pro Glu Met
340 345 350

Asp Asp Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Glu
355 360 365

Arg Gln Leu Ala Val Leu Val Ala Phe Ser Ser Val Thr Asn Gln Gly

370

375

380

Leu Pro Val Thr Pro Thr Phe Trp Arg Val Val Arg Phe Leu Ser Pro
385 390 395 400

Pro Ala Leu Gln Gly Tyr Val Ala Trp Leu Arg Ala Met Phe Leu Gln
405 410 415

Pro Asp Leu Asp Ser Leu Val Asp Phe Ser Thr Asn Asn Gln Lys Lys
420 425 430

Ala Gln Asp Ser Ser Leu His Met Pro Glu Arg Ala Val Phe Arg Leu
435 440 445

Arg Lys Trp Ile Ile Phe Arg Leu Val Ser Ile Val Asp Ser Leu His
450 455 460

Leu Glu Met Glu Glu Ala Leu Thr Glu Gln Val Ala Arg Phe Cys Leu
465 470 475 480

Phe His Ser Phe Phe Val Thr Lys Lys Pro Thr Ser Gln Ile Pro Glu
485 490 495

Thr Lys His Pro Phe Ser Phe Pro Leu Glu Asn Gln Ala Arg Glu Ala
500 505 510

Val Ser Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Thr Gln Phe
515 520 525

Lys Gln Ala Pro Gly Gln Thr Gln Gly Gly Gln Pro Trp Thr Tyr His
530 535 540

Leu Val Gln Phe Ala Asp Leu Leu Leu Asn His Ser His Asn Val Thr
545 550 555 560

Thr Val Thr Pro Phe Thr Ala Gln Gln His Gln Ala Trp Asp Arg Met
565 570 575

Leu Gln Thr Leu Lys Glu Leu Glu Ala His Ser Ala Glu Ala Arg Ala
580 585 590

Ala Ala Phe Gln His Leu Leu Leu Phe Val Gly Ile His Leu Leu Lys
595 600 605

Ser Pro Ala Glu Ser Cys Asp Leu Leu Gly Asp Ile Gln Thr Cys Ile

610

615

620

Arg Lys Ser Leu Gly Glu Lys Pro Arg Arg Ser Arg Thr Lys Thr Ile
625 630 635 640

Asp Pro Gln Glu Pro Pro Trp Val Glu Val Leu Val Glu Ile Leu Leu
645 650 655

Ala Leu Leu Ala Gln Pro Ser His Leu Met Arg Gln Val Ala Arg Ser
660 665 670

Val Phe Gly His Ile Cys Ser His Leu Thr Pro Arg Ala Leu Gln Leu
675 680 685

Ile Leu Asp Val Leu Asn Pro Glu Thr Ser Glu Asp Glu Asn Asp Arg
690 695 700

Val Val Val Thr Asp Asp Ser Asp Glu Arg Arg Leu Lys Gly Ala Glu
705 710 715 720

Asp Lys Ser Glu Glu Gly Glu Asp Asn Arg Ser Ser Glu Ser Glu Glu
725 730 735

Glu Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Arg Asp Gly Asp Val
740 745 750

Asp Gln Gly Phe Arg Glu Gln Leu Met Thr Val Leu Gln Ala Gly Lys
755 760 765

Ala Leu Gly Gly Glu Asp Ser Glu Asn Glu Glu Leu Gly Asp Glu
770 775 780

Ala Met Met Ala Leu Asp Gln Ser Leu Ala Ser Leu Phe Ala Glu Gln
785 790 795 800

Lys Leu Arg Ile Gln Ala Arg Arg Asp Glu Lys Asn Lys Leu Gln Lys
805 810 815

Glu Lys Ala Leu Arg Arg Asp Phe Gln Ile Arg Val Leu Asp Leu Val
820 825 830

Glu Val Leu Val Thr Lys Gln Pro Glu Asn Ala Leu Val Leu Glu Leu
835 840 845

Leu Glu Pro Leu Leu Ser Ile Ile Arg Arg Ser Leu Arg Ser Ser Ser

850

855

860

Ser Lys Gln Glu Gln Asp Leu Leu His Lys Thr Ala Arg Ile Phe Thr
865 870 875 880

His His Leu Cys Arg Ala Arg Arg Tyr Cys His Asp Leu Gly Glu Arg
885 890 895

Ala Gly Ala Leu His Ala Gln Val Glu Arg Leu Val Gln Gln Ala Gly
900 905 910

Arg Gln Pro Asp Ser Pro Thr Ala Leu Tyr His Phe Asn Ala Ser Leu
915 920 925

Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Ala Glu Gly Cys Val His
930 935 940

Glu Thr Gln Glu Lys Gln Lys Ala Gly Thr Asp Pro Ser His Met Pro
945 950 955 960

Thr Gly Pro Gln Ala Ala Ser Cys Leu Asp Leu Asn Leu Val Thr Arg
965 970 975

Val Tyr Ser Thr Ala Leu Ser Ser Phe Leu Thr Lys Arg Asn Ser Pro
980 985 990

Leu Thr Val Pro Met Phe Leu Ser Leu Phe Ser Arg His Pro Val Leu
995 1000 1005

Cys Gln Ser Leu Leu Pro Ile Leu Val Gln His Ile Thr Gly Pro
1010 1015 1020

Val Arg Pro Arg His Gln Ala Cys Leu Leu Leu Gln Lys Thr Leu
1025 1030 1035

Ser Met Arg Glu Val Arg Ser Cys Phe Glu Asp Pro Glu Trp Lys
1040 1045 1050

Gln Leu Met Gly Gln Val Leu Ala Lys Val Thr Glu Asn Leu Arg
1055 1060 1065

Val Leu Gly Glu Ala Gln Thr Lys Ala Gln His Gln Gln Ala Leu
1070 1075 1080

Ser Ser Leu Glu Leu Leu Asn Val Leu Phe Arg Thr Cys Lys His
106/168

1085

1090

1095

Glu Lys Leu Thr Leu Asp Leu Thr Val Leu Leu Gly Val Leu Gln
1100 1105 1110

Gly Gln Gln Gln Ser Leu Gln Gln Gly Ala His Ser Thr Gly Ser
1115 1120 1125

Ser Arg Leu His Asp Leu Tyr Trp Gln Ala Met Lys Thr Leu Gly
1130 1135 1140

Val Gln Arg Pro Lys Leu Glu Lys Lys Asp Ala Lys Glu Ile Pro
1145 1150 1155

Ser Ala Thr Gln Ser Pro Ile Ser Lys Lys Arg Lys Lys Lys Gly
1160 1165 1170

Phe Leu Pro Glu Thr Lys Lys Arg Lys Lys Arg Lys Ser Glu Asp
1175 1180 1185

Gly Thr Pro Ala Glu Asp Gly Thr Pro Ala Ala Thr Gly Gly Ser
1190 1195 1200

Gln Pro Pro Ser Met Gly Arg Lys Lys Arg Asn Arg Thr Lys Ala
1205 1210 1215

Lys Val Pro Ala Gln Ala Asn Gly Thr Pro Thr Thr Lys Ser Pro
1220 1225 1230

Ala Pro Gly Ala Pro Thr Arg Ser Pro Ser Thr Pro Ala Lys Ser
1235 1240 1245

Pro Lys Leu Gln Lys Lys Asn Gln Lys Pro Ser Gln Val Asn Gly
1250 1255 1260

Ala Pro Gly Ser Pro Thr Glu Pro Ala Gly Gln Lys Gln His Gln
1265 1270 1275

Lys Ala Leu Pro Lys Lys Gly Val Leu Gly Lys Ser Pro Leu Ser
1280 1285 1290

Ala Leu Ala Arg Lys Lys Ala Arg Leu Ser Leu Val Ile Arg Ser
1295 1300 1305

Pro Ser Leu Leu Gln Ser Gly Ala Lys Lys Lys Ala Gln Val Arg

1310

1315

1320

Lys Ala Gly Lys Pro
1325

<210> 35
<211> 2427
<212> DNA
<213> human

<220>
<221> CDS
<222> (86)..(1681)

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ctg gag cga tgc ctt agg ata tta ccc cat cat cag aat act gga ggg Leu Glu Arg Cys Leu Arg Ile Leu Pro His His Gln Asn Thr Gly Gly 170 175 180 185	640
ttt ttt gtg gca gta ttg gtg aaa aaa tct tca atg ccg tgg aat aaa Phe Phe Val Ala Val Leu Val Lys Lys Ser Ser Met Pro Trp Asn Lys 190 195 200	688
cgt cag cca aag ctt cag ggt aaa tct gca gag acc aga gaa agc aca Arg Gln Pro Lys Leu Gln Gly Lys Ser Ala Glu Thr Arg Glu Ser Thr 205 210 215	736
cag ctg agc cct gca gat ctc aca gaa ggg aaa ccc aca gat ccc tct Gln Leu Ser Pro Ala Asp Leu Thr Glu Gly Lys Pro Thr Asp Pro Ser 220 225 230	784
aag ctg gaa agt ccg tca ttc aca gga act ggt gac aca gaa ata gct Lys Leu Glu Ser Pro Ser Phe Thr Gly Thr Gly Asp Thr Glu Ile Ala 235 240 245	832
cat gca act gag gat tta gag aat aat ggc agt aag aaa gat ggc gtg His Ala Thr Glu Asp Leu Glu Asn Asn Gly Ser Lys Lys Asp Gly Val 250 255 260 265	880
tgt ggt cct cct cca tca aag aaa atg aag tta ttt gga ttt aaa gaa Cys Gly Pro Pro Pro Ser Lys Lys Met Lys Leu Phe Gly Phe Lys Glu 270 275 280	928
gat cca ttt gta ttt att cct gaa gat gac cca tta ttt cca cct att Asp Pro Phe Val Phe Ile Pro Glu Asp Asp Pro Leu Phe Pro Pro Ile 285 290 295	976
gag aaa ttt tat gct ttg gat cct tca ttc cca agg atg aat ttg tta Glu Lys Phe Tyr Ala Leu Asp Pro Ser Phe Pro Arg Met Asn Leu Leu 300 305 310	1024
act cg ^g act aca gaa ggg aag aaa agg cag ctc tac atg gtt tct aag Thr Arg Thr Thr Glu Gly Lys Lys Arg Gln Leu Tyr Met Val Ser Lys 315 320 325	1072
gag ttg cg ^g aat gtg ctg ctg aat aac agt gag aag atg aag gtt att Glu Leu Arg Asn Val Leu Leu Asn Asn Ser Glu Lys Met Lys Val Ile 330 335 340 345	1120
aac acg ggg atc aaa gtc tgg tgt aga aat aac agc ggt gaa gag ttt Asn Thr Gly Ile Lys Val Trp Cys Arg Asn Asn Ser Gly Glu Glu Phe 350 355 360	1168
gac tgt gct ttc cg ^g ctg gca cag gag gga ata tat aca ttg tat cca Asp Cys Ala Phe Arg Leu Ala Gln Glu Gly Ile Tyr Thr Leu Tyr Pro 365 370 375	1216
ttt att aac tca aga att att act gta tca atg gaa gat gtt aag ata Phe Ile Asn Ser Arg Ile Ile Thr Val Ser Met Glu Asp Val Lys Ile 380 385 390	1264

ctg ttg acc cag gaa aat ccc ttt ttt aga aaa ctc agc agt gag acc Leu Leu Thr Gln Glu Asn Pro Phe Phe Arg Lys Leu Ser Ser Glu Thr 395 400 405	1312
tac agt caa gca aag gac ctg gca aag gga agc atc gtg ctg aag tat Tyr Ser Gln Ala Lys Asp Leu Ala Lys Gly Ser Ile Val Leu Lys Tyr 410 415 420 425	1360
gaa cca gat tct gcg aat cca gac gct cta cag tgt ccc atc gtc tta Glu Pro Asp Ser Ala Asn Pro Asp Ala Leu Gln Cys Pro Ile Val Leu 430 435 440	1408
tgc gga tgg cgg gga aag gcc tcc att cga act ttt gtg ccc aag aat Cys Gly Trp Arg Gly Lys Ala Ser Ile Arg Thr Phe Val Pro Lys Asn 445 450 455	1456
gaa cgg ctt cac tat ctc agg atg atg ggg ctg gag gta ttg gga gaa Glu Arg Leu His Tyr Leu Arg Met Met Gly Leu Glu Val Leu Gly Glu 460 465 470	1504
aag aag aag gaa ggg gtt atc ctc aca aat gag agt gca gcc agc acc Lys Lys Glu Gly Val Ile Leu Thr Asn Glu Ser Ala Ala Ser Thr 475 480 485	1552
gga cag cca gac aat gac gtg act gag gga cag aga gca gga gag ccc Gly Gln Pro Asp Asn Asp Val Thr Glu Gly Gln Arg Ala Gly Glu Pro 490 495 500 505	1600
aac agc cca gat gca gaa gag gcc aac agt cca gac gtg aca gca ggc Asn Ser Pro Asp Ala Glu Glu Ala Asn Ser Pro Asp Val Thr Ala Gly 510 515 520	1648
tgt gac ccg gcg ggg gtc cat cca ccc cg ^g tga gcaggccaa ggcagcgggg Cys Asp Pro Ala Gly Val His Pro Pro Arg 525 530	1701
gcccacaccc ctcacacgca aaactggctt cttctggta ctgggtctg aaaccaaatc cagagcagcc tgtggctgt aaagcatata tttctagtga ctgcagactg gtggatcat aggagccttc tgaatgacca ggactgc ^t ttt cttggagct gatgaaaatg tactcttta gcgtgttaga aatca ^t ttgt tttat ^t ttgt tttcttggc caagctgggt ctatgtttc tttgctggg aatagacttt caaaagtgt acttctatca agaaacaaaa ctgc ^c ttgc agaaatttca ggtctttgt taagcctgta ttggcttaa ggtgcagtat ttttaaatt attatttata gaaagaatct ataaattttt gggaaagtgt gttataagct ttaataatta cattgagctg cacctcagtg gtgtgtcatt aacatgcagt ggggttaata tctgaggcct cagatgactt tgtgc ^c ttt ggaataaagg gtaaaataaa ctctcccaga gtaagagctg tatcgtgaat tgtcataacta attattgagg gggacttatg tgcttttatt gaatggagtg cttacaatt tttat ^t ttta aatggggttg ggatccttgg aatattcaa taaaattgat aaaatataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2421	1761 1821 1881 1941 2001 2061 2121 2181 2241 2301 2361

aaaaaa

2427

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<211> 531
<212> PRT
<213> human

<400> 36

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Val Asp Gly Arg Lys Glu Ile Leu Phe Tyr Asp Arg Ile Leu Cys Asp
20 25 30

Val Pro Cys Ser Gly Asp Gly Thr Met Arg Lys Asn Ile Asp Val Trp
35 40 45

Lys Lys Trp Thr Thr Leu Asn Ser Leu Gln Leu His Gly Leu Gln Leu
50 55 60

Arg Ile Ala Thr Arg Gly Ala Glu Gln Leu Ala Glu Gly Gly Arg Val
65 70 75 80

Val Tyr Ser Thr Cys Ser Leu Asn Pro Ile Glu Asp Glu Ala Val Ile
85 90 95

Ala Ser Leu Leu Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val
100 105 110

Ser Asn Glu Leu Pro Gly Leu Lys Trp Met Pro Gly Ile Thr Gln Trp
115 120 125

Lys Val Met Thr Lys Asp Gly Gln Trp Phe Thr Asp Trp Asp Ala Val
130 135 140

Pro His Ser Arg His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Lys
145 150 155 160

Asp Pro Glu Lys Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile
165 170 175

Leu Pro His His Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val
180 185 190

Lys Lys Ser Ser Met Pro Trp Asn Lys Arg Gln Pro Lys Leu Gln Gly
195 200 205

Lys Ser Ala Glu Thr Arg Glu Ser Thr Gln Leu Ser Pro Ala Asp Leu
210 215 220

Thr Glu Gly Lys Pro Thr Asp Pro Ser Lys Leu Glu Ser Pro Ser Phe
225 230 235 240

Thr Gly Thr Gly Asp Thr Glu Ile Ala His Ala Thr Glu Asp Leu Glu
245 250 255

Asn Asn Gly Ser Lys Lys Asp Gly Val Cys Gly Pro Pro Pro Ser Lys
260 265 270

Lys Met Lys Leu Phe Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro
275 280 285

Glu Asp Asp Pro Leu Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp
290 295 300

Pro Ser Phe Pro Arg Met Asn Leu Leu Thr Arg Thr Thr Glu Gly Lys
305 310 315 320

Lys Arg Gln Leu Tyr Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu
325 330 335

Asn Asn Ser Glu Lys Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp
340 345 350

Cys Arg Asn Asn Ser Gly Glu Glu Phe Asp Cys Ala Phe Arg Leu Ala
355 360 365

Gln Glu Gly Ile Tyr Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile
370 375 380

Thr Val Ser Met Glu Asp Val Lys Ile Leu Leu Thr Gln Glu Asn Pro
385 390 395 400

Phe Phe Arg Lys Leu Ser Ser Glu Thr Tyr Ser Gln Ala Lys Asp Leu
405 410 415

Ala Lys Gly Ser Ile Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro
420 425 430

Asp Ala Leu Gln Cys Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala
435 440 445

Ser Ile Arg Thr Phe Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg
450 455 460

Met Met Gly Leu Glu Val Leu Gly Glu Lys Lys Lys Glu Gly Val Ile
465 470 475 480

/
Leu Thr Asn Glu Ser Ala Ala Ser Thr Gly Gln Pro Asp Asn Asp Val
485 490 495

Thr Glu Gly Gln Arg Ala Gly Glu Pro Asn Ser Pro Asp Ala Glu Glu
500 505 510

Ala Asn Ser Pro Asp Val Thr Ala Gly Cys Asp Pro Ala Gly Val His
515 520 525

Pro Pro Arg
530

<210> 37
<211> 1792
<212> DNA
<213> human

<220>
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<222> (61)..(1281)

<400> 37
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atg ggg ccc agc acc cct ctc atc ttg ttc ctt ttg tca tgg tcg 108
Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
1 5 10 15

gga ccc ctc caa gga cag cag cac cac ctt gtg gag tac atg gaa cgc 156
Gly Pro Leu Gln Gly Gln His His Leu Val Glu Tyr Met Glu Arg
20 25 30

cga cta gct gct tta gag gaa cgg ctg gcc cag tgc cag gac cag agt 204
Arg Leu Ala Ala Leu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
35 40 45

agt cgg cat gct gag ctg cgg gac ttc aag aac aag atg ctg cca 252
Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
50 55 60

ctg ctg gag gtg gca gag aag gag cgg gag gca ctc aga act gag gcc 300
Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
65 70 75 80

gac acc atc tcc ggg aga gtg gat cgt ctg gag cgg gag gta gac tat 348

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr			
85	90	95	
ctg gag acc cag aac cca gct ctg ccc tgt gta gag ttt gat gag aag			396
Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys			
100	105	110	
gtg act gga ggc cct ggg acc aaa ggc aag gga aga agg aat gag aag			444
Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys			
115	120	125	
tac gat atg gtg aca gac tgt ggc tac aca atc tct caa gtg aga tca			492
Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser			
130	135	140	
atg aag att ctg aag cga ttt ggt ggc cca gct ggt cta tgg acc aag			540
Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys			
145	150	155	160
gat cca ctg ggg caa aca gag aag atc tac gtg tta gat ggg aca cag			588
Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln			
165	170	175	
aat gac aca gcc ttt gtc ttc cca agg ctg cgt gac ttc acc ctt gcc			636
Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala			
180	185	190	
atg gct gcc cgaa gct tcc cga gtc cggt gtg ccc ttc ccc tgg gta			684
Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val			
195	200	205	
ggc aca ggg cag ctg gta tat ggt ggc ttt ctt tat ttt gct cgg agg			732
Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg			
210	215	220	
cct cct gga aga cct ggt gga ggt gag atg gag aac act ttg cag			780
Pro Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln			
225	230	235	240
cta atc aaa ttc cac ctg gca aac cga aca gtg gtg gac agc tca gta			828
Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val			
245	250	255	
ttc cca gca gag ggg ctg atc ccc ccc tac ggc ttg aca gca gac acc			876
Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr			
260	265	270	
tac atc gac ctg gca gct gat gag gaa ggt ctt tgg gct gtc tat gcc			924
Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala			
275	280	285	
acc cgg gag gat gac agg cac ttg tgt ctg gcc aag tta gat cca cag			972
Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln			
290	295	300	
aca ctg gac aca gag cag cag tgg gac aca cca tgt ccc aga gag aat			1020
Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn			
305	310	315	320
gct gag gct gcc ttt gtc atc tgt ggg acc ctc tat gtc gtc tat aac			1068

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn			
325	330	335	
acc cgt cct gcc agt cg ^g gcc cgc atc cag tgc tcc ttt gat gcc agc			1116
Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser			
340	345	350	
ggc acc ctg acc cct gaa cg ^g gca gca ctc cct tat ttt ccc cgc aga			1164
Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg			
355	360	365	
tat ggt gcc cat gcc agc ctc cgc tat aac ccc cga gaa cgc cag ctc			1212
Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu			
370	375	380	
tat gcc tgg gat gat ggc tac cag att gtc tat aag ctg gag atg agg			1260
Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg			
385	390	395	400
aag aaa gag gag gag gtt tga ggagctagcc ttgtttttg catctttctc			1311
Lys Lys Glu Glu Val			
405			
actccccatac atttatatta tatccccact aaatttcttg ttccctcatc ttcaaatgtg			1371
ggccagttgt ggctcaaatc ctctatattt ttagccaatg gcaatcaaat tctttcagct			1431
cctttgttcc atacggaact ccagatcctg agtaatcctt ttagagcccg aagagtcaaa			1491
accctcaatg ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc			1551
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc agcagtgttc			1611
ttccccctcag agtgacttgg ggagggagaa ataggaggag acgtccagct ctgtcctctc			1671
ttcctcactc ctcccttcag tgtcctgagg aacaggactt tctccacatt gttttgtatt			1731
gcaacatttt gcattaaaag gaaaatccac tgctaaaaaaaaaaaaaaaaaaaaaaa			1791
a			1792

<210> 38
<211> 406
<212> PRT
<213> human

<400> 38

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
1 5 10 15

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
20 25 30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
35 40 45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
50 55 60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
65 70 75 80

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys
100 105 110

Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys
115 120 125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser
130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys
145 150 155 160

Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
165 170 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
180 185 190

Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val
195 200 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg
210 215 220

Pro Pro Gly Arg Pro Gly Gly Glu Met Glu Asn Thr Leu Gln
225 230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
245 250 255

Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
260 265 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
275 280 285

Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
290 295 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
305 310 315 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
325 330 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
340 345 350

Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg
355 360 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
370 375 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg
385 390 395 400

Lys Lys Glu Glu Val
405

<210> 39
<211> 1925
<212> DNA
<213> human

<220>
<221> CDS
<222> (127) .. (1278)

<400> 39
agtggagtgg gacaggtata taaaggaagt acagggcctg gggaaaggagc cctgtctagg 60
tagctggcac caggagccgt gggcaaggga agaggccaca ccctgccttg ctctgctgca 120
gccaga atg ggt gtg aag gcg tct caa aca ggc ttt gtg gtc ctg gtg 168
Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val
1 5 10

ctg ctc cag tgc tgc tct gca tac aaa ctg gtc tgc tac tac acc agc 216
Leu Leu Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser
15 20 25 30

tgg tcc cag tac cgg gaa ggc gat ggg agc tgc ttc cca gat gcc ctt 264
Trp Ser Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu
35 40 45

gac cgc ttc ctc tgt acc cac atc atc tac agc ttt gcc aat ata agc Asp Arg Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser 50 55 60	312
aac gat cac atc gac acc tgg gag tgg aat gat gtg acg ctc tac ggc Asn Asp His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly 65 70 75	360
atg ctc aac aca ctc aag aac agg aac ccc aac ctg aag act ctc ttg Met Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu 80 85 90	408
tct gtc gga gga tgg aac ttt ggg tct caa aga ttt tcc aag ata gcc Ser Val Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala 95 100 105 110	456
tcc aac acc cag agt cgc cgg act ttc atc aag tca gta ccg cca ttc Ser Asn Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe 115 120 125	504
ctg cgc acc cat ggc ttt gat ggg ctg gac ctt gcc tgg ctc tac cct Leu Arg Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro 130 135 140	552
gga cgg aga gac aaa cag cat ttt acc acc cta atc aag gaa atg aag Gly Arg Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys 145 150 155	600
gcc gaa ttt ata aag gaa gcc cag cca ggg aaa aag cag ctc ctg ctc Ala Glu Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu 160 165 170	648
agc gca gca ctg tct gcg ggg aag gtc acc att gac agc agc tat gac Ser Ala Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp 175 180 185 190	696
att gcc aag ata tcc caa cac ctg gat ttc att agc atc atg acc tac Ile Ala Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr 195 200 205	744
gat ttt cat gga gcc tgg cgt ggg acc aca ggc cat cac agt ccc ctg Asp Phe His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu 210 215 220	792
ttc cga ggt cag gag gat gca agt cct gac aga ttc agc aac act gac Phe Arg Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp 225 230 235	840
tat gct gtg ggg tac atg ttg agg ctg ggg gct cct gcc agt aag ctg Tyr Ala Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu 240 245 250	888
gtg atg ggc atc ccc acc ttc ggg agg agc ttc act ctg gct tct tct Val Met Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser 255 260 265 270	936
gag act ggt gtt gga gcc cca atc tca gga ccg gga att cca ggc cgg Glu Thr Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg 275 280 285	984

ttc acc aag gag gca ggg acc ctt gcc tac tat gag atc tgt gac ttc		1032	
Phe Thr Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe			
290	295	300	
ctc cgc gga gcc aca gtc cat aga acc ctc ggc cag cag gtc ccc tat		1080	
Leu Arg Gly Ala Thr Val His Arg Thr Leu Gly Gln Gln Val Pro Tyr			
305	310	315	
gcc acc aag ggc aac cag tgg gta gga tac gac gac cag gaa agc gtc		1128	
Ala Thr Lys Gly Asn Gln Trp Val Gly Tyr Asp Asp Gln Glu Ser Val			
320	325	330	
aaa agc aag gtg cag tac ctg aag gat agg cag ctg gca ggc gcc atg		1176	
Lys Ser Lys Val Gln Tyr Leu Lys Asp Arg Gln Leu Ala Gly Ala Met			
335	340	345	350
gta tgg gcc ctg gac ctg gat gac ttc cag ggc tcc ttc tgc ggc cag		1224	
Val Trp Ala Leu Asp Leu Asp Asp Phe Gln Gly Ser Phe Cys Gly Gln			
355	360	365	
gat ctg cgc ttc cct ctc acc aat gcc atc aag gat gca ctc gct gca		1272	
Asp Leu Arg Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala Ala			
370	375	380	
acg tag ccctctgttc tgcacacacgc acgggggcca aggatgcccc gtcccccct		1328	
Thr			
ggctccagct ggccgggagc ctgatcacct gccctgctga gtcccaggct gagcctcagt		1388	
ctccctccct tggggcctat gcagagggcc acaacacaca gattttagct cagccctgg		1448	
gggcagagag gtagggatgg ggctgtgggg atagtgaggc atcgcaatgt aagactcggg		1508	
attagtacac acttgttcat gattaatggg aatgtttaca gatccccaaag cctggcaagg		1568	
gaatttcttc aactccctgc cccctagccc tccttatcaa aggacaccat tttggcaagc		1628	
tctatcacca aggagccaaa catcctacaa gacacagtga ccatactaata tataccccct		1688	
gcaaagccag cttgaaacct tcacttagga acgtaatcgt gtcccctatc ctacttcccc		1748	
ttcctaattc cacagctgct caataaagta caagagtttta acagtgtgtt ggcgctttgc		1808	
tttggtctat cttttagcgc ccactagacc cactggactc acctccccca tctttctgg		1868	
gttccttcct ctgagccttg ggaccctga gcttgcagag atgaaggccg ccatgtt		1925	

<210> 40
<211> 383
<212> PRT
<213> human

<400> 40

Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val Leu Leu			
1	5	10	15

Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser
20 25 30

Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu Asp Arg
35 40 45

Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Asn Asp
50 55 60

His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly Met Leu
65 70 75 80

Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser Val
85 90 95

Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala Ser Asn
100 105 110

Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe Leu Arg
115 120 125

Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Gly Arg
130 135 140

Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys Ala Glu
145 150 155 160

Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu Ser Ala
165 170 175

Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp Ile Ala
180 185 190

Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr Asp Phe
195 200 205

His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu Phe Arg
210 215 220

Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp Tyr Ala
225 230 235 240

Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu Val Met
245 250 255

Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser Glu Thr
260 265 270

Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg Phe Thr
275 280 285

Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu Arg
290 295 300

Gly Ala Thr Val His Arg Thr Leu Gly Gln Gln Val Pro Tyr Ala Thr
305 310 315 320

Lys Gly Asn Gln Trp Val Gly Tyr Asp Asp Gln Glu Ser Val Lys Ser
325 330 335

Lys Val Gln Tyr Leu Lys Asp Arg Gln Leu Ala Gly Ala Met Val Trp
340 345 350

Ala Leu Asp Leu Asp Asp Phe Gln Gly Ser Phe Cys Gly Gln Asp Leu
355 360 365

Arg Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala Ala Thr
370 375 380

<210> 41
<211> 2105
<212> DNA
<213> human

<220>
<221> CDS
<222> (235)..(1752)

<400> 41
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aggacgagaa acgccccggg caccaaagcc cctcagagcg tcgccccccgc ctctagttct 120
agaaaagtcaag tttcccgcca ctggcaccccc ggaacctcaag gggctgccga gctggggggg 180
cgctcaagct gcgaggatcc gggctgcccg cgagacgagg agcgggcgcc cagg atg 237
Met
1

ggg tgc atg aag tcc aag ttc ctc cag gtc gga ggc aat aca ttc tca 285
Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe Ser
5 10 15

aaa act gaa acc agc gcc agc cca cac tgt cct gtg tac gtg ccg gat 333
Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro Asp
20 25 30

ccc aca tcc acc atc aag ccg ggg cct aat agc cac aac agc aac aca		381	
Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn Thr			
35	40	45	
cca gga atc agg gag gca ggc tct gag gac atc atc gtg gtt gcc ctg		429	
Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu			
50	55	60	65
tat gat tac gag gcc att cac cac gaa gac ctc agc ttc cag aag ggg		477	
Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly			
70	75	80	
gac cag atg gtg gtc cta gag gaa tcc ggg gag tgg tgg aag gct cga		525	
Asp Gln Met Val Val Leu Glu Ser Gly Glu Trp Trp Lys Ala Arg			
85	90	95	
tcc ctg gcc acc cgg aag gag ggc tac atc cca agc aac tat gtc gcc		573	
Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala			
100	105	110	
cgc gtt gac tct ctg gag aca gag gag tgg ttt ttc aag ggc atc agc		621	
Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser			
115	120	125	
cgg aag gac gca gag cgc caa ctg ctg gct ccc ggc aac atg ctg ggc		669	
Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu Gly			
130	135	140	145
tcc ttc atg atc cgg gat agc gag acc act aaa gga agc tac tct ttg		717	
Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu			
150	155	160	
tcc gtg cga gac tac gac cct cgg cag gga gat acc gtg aaa cat tac		765	
Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His Tyr			
165	170	175	
aag atc cgg acc ctg gac aac ggg ggc ttc tac ata tcc ccc cga agc		813	
Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg Ser			
180	185	190	
acc ttc agc act ctg cag gag ctg gtg gac cac tac aag aag ggg aac		861	
Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly Asn			
195	200	205	
gac ggg ctc tgc cag aaa ctg tcg gtg ccc tgc atg tct tcc aag ccc		909	
Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys Pro			
210	215	220	225
cag aag cct tgg gag aaa gat gcc tgg gag atc cct cgg gaa tcc ctc		957	
Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu			
230	235	240	
aag ctg gag aag aaa ctt gga gct ggg cag ttt ggg gaa gtc tgg atg		1005	
Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met			
245	250	255	
gcc acc tac aac aag cac acc aag gtg gca gtg aag acg atg aag cca		1053	
Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro			
260	265	270	

ggg agc atg tcg gtg gag gcc ttc ctg gca gag gcc aac gtg atg aaa		1101	
Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met Lys			
275	280	285	
act ctg cag cat gac aag ctg gtc aaa ctt cat gcg gtg gtc acc aag		1149	
Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr Lys			
290	295	300	305
gag ccc atc tac atc acg gag ttc atg gcc aaa gga agc ttg ctg		1197	
Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu Leu			
310	315	320	
gac ttt ctg aaa agt gat gag ggc agc aag cag cca ttg cca aaa ctc		1245	
Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu			
325	330	335	
att gac ttc tca gcc cag att gca gaa ggc atg gcc ttc atc gag cag		1293	
Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln			
340	345	350	
agg aac tac atc cac cga gac ctc cga gct gcc aac atc ttg gtc tct		1341	
Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser			
355	360	365	
gca tcc ctg gtg tgt aag att gct gac ttt ggc ctg gcc cgg gtc att		1389	
Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile			
370	375	380	385
gag gac aac gag tac acg gct cgg gaa ggg gcc aag ttc ccc atc aag		1437	
Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys			
390	395	400	
tgg aca gct cct gaa gcc atc aac ttt ggc tcc ttc acc atc aag tca		1485	
Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser			
405	410	415	
gac gtc tgg tcc ttt ggt atc ctg ctg atg gag atc gtc acc tac ggc		1533	
Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly			
420	425	430	
cgg atc cct tac cca ggg atg tca aac cct gaa gtg atc cga gct ctg		1581	
Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu			
435	440	445	
gag cgt gga tac cgg atg cct cgc cca gag aac tgc cca gag gag ctc		1629	
Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu Leu			
450	455	460	465
tac aac atc atg atg cgc tgc tgg aaa aac cgt ccg gag gag cgg ccg		1677	
Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro			
470	475	480	
acc ttc gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc aca		1725	
Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr			
485	490	495	
gag agc cag tac caa cag cag cca tga tagggaggac cagggcaggg		1772	
Glu Ser Gln Tyr Gln Gln Pro			
500	505		

ccagggggtg cccaggtggt ggctgcaagg tggctccagc accatccgcc agggcccaca 1832
cccccttcct actcccagac acccaccctc gcttcagcca cagttcctc atctgtccag 1892
tggtaggtt ggactggaaa atctctttt gactcttgca atccacaatc tgacattctc 1952
aggaagcccc caagttgata tttctatttc ctggaatggg tggattttag ttacagctgt 2012
gatttggaaag ggaaactttc aaaatagtga aatgaatatt taaataaaag atataaatgc 2072
caaagtcttt accaaaaaaaaaaaaaaa aaa 2105

<210> 42
<211> 505
<212> PRT
<213> human

<400> 42

Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
1 5 10 15

Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
20 25 30

Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
35 40 45

Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala
50 55 60

Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys
65 70 75 80

Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala
85 90 95

Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val
100 105 110

Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile
115 120 125

Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu
130 135 140

Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser
145 150 155 160

Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
165 170 175

Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
180 185 190

Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
195 200 205

Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
210 215 220

Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
225 230 235 240

Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
245 250 255

Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
260 265 270

Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
275 280 285

Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
290 295 300

Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
305 310 315 320

Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
325 330 335

Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
340 345 350

Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
355 360 365

Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
370 375 380

Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
385 390 395 400

Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
405 410 415

Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
420 425 430

Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
435 440 445

Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
450 455 460

Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
465 470 475 480

Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
485 490 495

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
500 505

<210> 43
<211> 3432
<212> DNA
<213> human

<220>
<221> CDS
<222> (248) . . . (2572)

<400> 43
actccagcgc gcggctacct acgcttggtg cttgtttct ccagccatcg gagaccagag 60
ccggccccctc tgctcgagaa aggggctcag cggcgccgga agcggagggg gaccaccgtg 120
gagagcgcgg tcccagcccg gccactgcgg atccctgaaa ccaaaaagct cctgctgctt 180
ctgtaccccg cctgtccctc ccagctgcgc agggccccctt cgtggatca tcagcccgaa 240
gacaggg atg gag agg cct ctg tgc tcc cac ctc tgc agc tgc ctg gct 289
Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala
1 5 10

atg ctg gcc ctc ctg tcc ccc ctg agc ctg gca cag tat gac agc tgg 337
Met Leu Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp
15 20 25 30

ccc cat tac ccc gag tac ttc cag caa ccg gct cct gag tat cac cag 385
Pro His Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln
35 40 45

ccc cag gcc ccc gcc aac gtg gcc aag att cag ctg cgc ctg gct ggg Pro Gln Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly	50	55	60	433
cag aag agg aag cac agc gag ggc cggtt gat gac gac ttc tcc atc cac gct gcc cac Gln Lys Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly	65	70	75	481
cag tgg ggc acc gtg tgc gat gac gac ttc tcc atc cac gct gcc cac Gln Trp Gly Thr Val Cys Asp Asp Phe Ser Ile His Ala Ala His	80	85	90	529
gtc gtc tgc cgg gag ctg ggc tat gtg gag gcc aag tcc tgg act gcc Val Val Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala	95	100	105	577
agc tcc tcc tac ggc aag gga gaa ggg ccc atc tgg tta gac aat ctc Ser Ser Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu	115	120	125	625
cac tgt act ggc aac gag gcg acc ctt gca gca tgc acc tcc aat ggc His Cys Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly	130	135	140	673
tgg ggc gtc act gac tgc aag cac acg gag gat gtc ggt gtg gtg tgc Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys	145	150	155	721
agc gac aaa agg att cct ggg ttc aaa ttt gac aat tcg ttg atc aac Ser Asp Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn	160	165	170	769
cag ata gag aac ctg aat atc cag gtg gag gac att cgg att cga gcc Gln Ile Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala	175	180	185	817
atc ctc tca acc tac cgc aag cgc acc cca gtg atg gag ggc tac gtg Ile Leu Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val	195	200	205	865
gag gtg aag gag ggc aag acc tgg aag cag atc tgt gac aag cac tgg Glu Val Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp	210	215	220	913
acg gcc aag aat tcc cgc gtg gtc tgc ggc atg ttt ggc ttc cct ggg Thr Ala Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly	225	230	235	961
gag agg aca tac aat acc aaa gtg tac aaa atg ttt gcc tca cgg agg Glu Arg Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg	240	245	250	1009
aag cag cgc tac tgg cca ttc tcc atg gac tgc acc ggc aca gag gcc Lys Gln Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala	255	260	265	1057
cac atc tcc agc tgc aag ctg ggc ccc cag gtg tca ctg gac ccc atg His Ile Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met	275	280	285	1105

aag aat gtc acc tgc gag aat ggg ctg ccg gcc gtg gtg agt tgt gtg Lys Asn Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val 290 295 300	1153
cct ggg cag gtc ttc agc cct gac gga ccc tcg aga ttc cgg aaa gca Pro Gly Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala 305 310 315	1201
tac aag cca gag caa ccc ctg gtg cga ctg aga ggc ggt gcc tac atc Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile 320 325 330	1249
ggg gag ggc cgc gtg gag gtg ctc aaa aat gga gaa tgg ggg acc gtc Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val 335 340 345 350	1297
tgc gac gac aag tgg gac ctg gtg tcg gcc agt gtg gtc tgc aga gag Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu 355 360 365	1345
ctg ggc ttt ggg agt gcc aaa gag gca gtc act ggc tcc cga ctg ggg Leu Gly Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly 370 375 380	1393
caa ggg atc gga ccc atc cac ctc aac gag atc cag tgc aca ggc aat Gln Gly Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn 385 390 395	1441
gag aag tcc att ata gac tgc aag ttc aat gcc gag tct cag ggc tgc Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys 400 405 410	1489
aac cac gag gag gat gct ggt gtg aga tgc aac acc cct gcc atg ggc Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly 415 420 425 430	1537
ttg cag aag aag ctg cgc ctg aac ggc ggc cgc aat ccc tac gag ggc Leu Gln Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly 435 440 445	1585
cga gtg gag gtg ctg gtg gag aga aac ggg tcc ctt gtg tgg ggg atg Arg Val Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met 450 455 460	1633
gtg tgt ggc caa aac tgg ggc atc gtg gag gcc atg gtg gtc tgc cgc Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg 465 470 475	1681
cag ctg ggc ctg gga ttc gcc agc aac gcc ttc cag gag acc tgg tat Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr 480 485 490	1729
tgg cac gga gat gtc aac agc aac aaa gtg gtc atg agt gga gtg aag Trp His Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys 495 500 505 510	1777
tgc tcg gga acg gag ctg tcc ctg gcg cac tgc cgc cac gac ggg gag Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu 515 520 525	1825

gac gtg gcc tgc ccc cag ggc gga gtg cag tac ggg gcc gga gtt gcc Asp Val Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala 530 535 540	1873
tgc tca gaa acc gcc cct gac ctg gtc ctc aat gcg gag atg gtg cag Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln 545 550 555	1921
cag acc acc tac ctg gag gac cgg ccc atg ttc atg ctg cag tgt gcc Gln Thr Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala 560 565 570	1969
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acg ggc tac cgc cgg ctc ctg cgc ttc tcc tcc cag atc cac aac aat Thr Gly Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn 595 600 605	2065
ggc cag tcc gac ttc cgg ccc aag aac ggc cgc cac gcg tgg atc tgg Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp 610 615 620	2113
cac gac tgt cac agg cac tac cac agc atg gag gtg ttc acc cac tat His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr 625 630 635	2161
gac ctg ctg aac ctc aat ggc acc aag gtg gca gag ggc cac aag gcc Asp Leu Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 640 645 650	2209
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gag gtt gca gaa tcc gat tac tcc aac aac atc atg aaa tgc agg agc Glu Val Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser 720 725 730	2449
cgc tat gac ggc cac cgc atc tgg atg tac aac tgc cac ata ggt ggt Arg Tyr Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly 735 740 745 750	2497
tcc ttc agc gaa gag acg gaa aaa aag ttt gag cac ttc agc ggg ctc Ser Phe Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu 755 760 765	2545

tta aac aac cag ctg tcc ccg cag taa agaaggcctgc gtggtcaact	2592
Leu Asn Asn Gln Leu Ser Pro Gln	
770	
cctgtcttca ggccacacca catcttccat gggacttccc cccaacaact gagtctgaac	2652
gaatgccacg tgccctcacc cagccccggcc cccaccctgt ccagaccctt acagctgtgt	2712
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20	25		30
	30		

Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln			
35	40		45
	45		

Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys			
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	60		

Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp					
65	70		75		80
	75				
	80				

Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His Val Val
85 90 95

Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser
100 105 110

Ser Tyr Gly Lys Gly Glu Pro Ile Trp Leu Asp Asn Leu His Cys
115 120 125

Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly
130 135 140

Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp
145 150 155 160

Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn Gln Ile
165 170 175

Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu
180 185 190

Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val
195 200 205

Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala
210 215 220

Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg
225 230 235 240

Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln
245 250 255

Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile
260 265 270

Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn
275 280 285

Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val Pro Gly
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Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala Tyr Lys
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Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu
325 330 335

Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp
340 345 350

Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly
355 360 365

Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly
370 375 380

Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys
385 390 395 400

Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His
405 410 415

Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln
420 425 430

Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val
435 440 445

Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys
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Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu
465 470 475 480

Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His
485 490 495

Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser
500 505 510

Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val
515 520 525

Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser
530 535 540

Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr
545 550 555 560

Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu
565 570 575

Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly
580 585 590

Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln
595 600 605

Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp
610 615 620

Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu
625 630 635 640

Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe
645 650 655

Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu
660 665 670

Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met
675 680 685

Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro
690 695 700

Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe Glu Val
705 710 715 720

Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser Arg Tyr
725 730 735

Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly Ser Phe
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ggaagagcct tccgcaggc cccgccccgt cacgtggcg ccggccccgg ccgctgcgg 180
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gctcgcttct gggctctcat gtttgaaggt gggagggaca cgggagcggc cccgacac 300
gagccgccccg gagaggagcc tcggccccgt acccagtaag aagaggagga ggccaggc 360
gcaaaaggag tc atg gct tct gat gct agt cat gcg ctg gaa gct gcc ctg 411
Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu
1 5 10

gag caa atg gac ggg atc att gca ggc act aaa aca ggt gca gat ctt 459
Glu Gln Met Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu
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agt gat ggt act tgt gag cct gga ctg gct tcc ccg gcc tcc tac atg 507
Ser Asp Gly Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met
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aac ccc ttc ccg gtg ctc cat ctc atc gag gac ttg agg ctg gcc ttg 555
Asn Pro Phe Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu
50 55 60

gag atg ctg gag ctt cct cag gag aga gca gcc ctc ctg agc cag atc 603
Glu Met Leu Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser Gln Ile
65 70 75

cct ggc cca aca gct gcc tac ata aag gaa tgg ttt gaa gag agc ttg 651
Pro Gly Pro Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu Glu Ser Leu
80 85 90

tcc cag gta aac cac cac agt gct gct agt aat gaa acc tac cag gaa 699
Ser Gln Val Asn His His Ser Ala Ala Ser Asn Glu Thr Tyr Gln Glu
95 100 105

cgc ttg gca cgt cta gaa ggg gat aag gag tcc ctc ata ttg cag gtg 747
Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val
110 115 120 125

agt gtc ctc aca gac caa gta gaa gcc cag gga gaa aag att cga gac 795
Ser Val Leu Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp
130 135 140

ctg gaa gtg tgt ctg gaa gga cac cag gtg aaa ctc aat gct gct gaa 843
Leu Glu Val Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu
145 150 155

gag atg ctt caa cag gag ctg cta agc cgc aca tct ctt gag acc cag 891

Glu	Met	Leu	Gln	Gln	Glu	Leu	Leu	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Gln	
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Lys	Leu	Asp	Leu	Met	Thr	Glu	Val	Ser	Glu	Leu	Lys	Leu	Lys	Leu	Val	
175					180					185						
ggc	atg	gag	aag	gag	cag	aga	gag	cag	gag	aag	cag	aga	aaa	gca		987
Gly	Met	Glu	Lys	Glu	Gln	Arg	Glu	Gln	Glu	Lys	Gln	Arg	Lys	Ala		
190			195						200			205				
gag	gag	tta	ctg	caa	gag	ctc	agg	cac	ctc	aaa	atc	aaa	gtg	gaa	gag	1035
Glu	Glu	Leu	Leu	Gln	Glu	Leu	Arg	His	Leu	Lys	Ile	Lys	Val	Glu	Glu	
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Leu	Glu	Asn	Glu	Arg	Asn	Gln	Tyr	Glu	Trp	Lys	Leu	Lys	Ala	Thr	Lys	
225								230					235			
gct	gaa	gtc	gcc	cag	ctg	caa	gaa	cag	gtg	gcc	ctg	aaa	gat	gca	gaa	1131
Ala	Glu	Val	Ala	Gln	Leu	Gln	Glu	Gln	Val	Ala	Leu	Lys	Asp	Ala	Glu	
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att	gag	cgt	ctg	cac	agc	cag	ctc	tcc	cgg	aca	gca	gct	ctc	cac	agt	1179
Ile	Glu	Arg	Leu	His	Ser	Gln	Leu	Ser	Arg	Thr	Ala	Ala	Leu	His	Ser	
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Glu	Ser	His	Thr	Glu	Arg	Asp	Gln	Glu	Ile	Gln	Arg	Leu	Lys	Met	Gly	
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Met	Glu	Thr	Leu	Leu	Leu	Ala	Asn	Glu	Asp	Lys	Asp	Arg	Arg	Ile	Glu	
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Glu	Pro	Glu	Gly	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Thr	Asn	Lys	Asp	Pro	
335								340					345			
gaa	gaa	tta	ttt	aaa	caa	gag	atg	cct	cca	aga	tgt	agc	tct	cct	aca	1467
Glu	Glu	Leu	Phe	Lys	Gln	Glu	Met	Pro	Pro	Arg	Cys	Ser	Ser	Pro	Thr	
350								355					360		365	
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Val	Gly	Pro	Pro	Pro	Leu	Pro	Gln	Lys	Ser	Leu	Glu	Thr	Arg	Ala	Gln	
370								375					380			
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Lys	Lys	Leu	Ser	Cys	Ser	Leu	Glu	Asp	Leu	Arg	Ser	Glu	Ser	Val	Asp	
385								390					395			
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Ser	Pro	Phe	Leu	Ala	Glu	His	Lys	Tyr	Pro	Thr	Leu	Pro	Gly	Lys	Leu	
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Ser	Gly	Ala	Thr	Pro	Asn	Gly	Glu	Ala	Ala	Lys	Ser	Pro	Pro	Thr	Ile	
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Cys	Gln	Pro	Asp	Ala	Thr	Gly	Ser	Ser	Leu	Leu	Arg	Leu	Arg	Asp	Thr	
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Glu	Ser	Gly	Trp	Asp	Asp	Thr	Ala	Val	Val	Asn	Asp	Leu	Ser	Ser	Thr	
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Lys	Arg	Asn	Pro	Lys	Gly	Ile	Lys	Lys	Phe	Trp	Gly	Lys	Ile	Arg	Arg	
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Thr	Gln	Ser	Gly	Asn	Phe	Tyr	Thr	Asp	Thr	Leu	Gly	Met	Ala	Glu	Phe	
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Arg	Arg	Gly	Gly	Leu	Arg	Ala	Thr	Ala	Gly	Pro	Arg	Leu	Ser	Arg	Thr	
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agg	gac	tcc	aag	gga	cag	aaa	agt	gac	gcc	aat	gcc	ccc	ttt	gcc	cag	2043
Arg	Asp	Ser	Lys	Gly	Gln	Lys	Ser	Asp	Ala	Asn	Ala	Pro	Phe	Ala	Gln	
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Trp	Ser	Thr	Glu	Arg	Val	Cys	Ala	Trp	Leu	Glu	Asp	Phe	Gly	Leu	Ala	
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Gln	Tyr	Val	Ile	Phe	Ala	Arg	Gln	Trp	Val	Ser	Ser	Gly	His	Thr	Leu	
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Leu	Thr	Ala	Thr	Pro	Gln	Asp	Met	Glu	Lys	Glu	Leu	Gly	Ile	Lys	His	
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cca	ctc	cac	agg	aag	aag	ctt	gtt	tta	gca	gtg	aaa	gcc	atc	aac	acc	2235
Pro	Leu	His	Arg	Lys	Lys	Leu	Val	Leu	Ala	Val	Lys	Ala	Ile	Asn	Thr	
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Lys	Gln	Glu	Glu	Lys	Ser	Ala	Leu	Leu	Asp	His	Ile	Trp	Val	Thr	Arg	
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Trp Leu Asp Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu			
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Ser Arg Val Asp Arg Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu			
655	660	665	
ctc ttc tta aaa gtc acc agc caa cta cat cat ctc agc atc aaa tgt		2427	
Leu Phe Leu Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys			
670	675	680	685
gcc att cac gtg ctg cat gtc aac aag ttc aac ccc cac tgc ctg cac		2475	
Ala Ile His Val Leu His Val Asn Lys Phe Asn Pro His Cys Leu His			
690	695	700	
cgg cgg cca gct gat gag agt aac ctt tct cct tca gaa gtt gta cag		2523	
Arg Arg Pro Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln			
705	710	715	
tgg tcc aac cac agg gtg atg gag tgg tta cga tct gtg gac ctg gca		2571	
Trp Ser Asn His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala			
720	725	730	
gag tat gca ccc aat ctt cga ggg agt gga gtc cat gga ggc ctc att		2619	
Glu Tyr Ala Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile			
735	740	745	
atc ctg gag cca cgc ttc act ggg gac acc ctg gct atg ctt ctc aac		2667	
Ile Leu Glu Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn			
750	755	760	765
atc ccc cca caa aag acg ctc ctc agg cgc cac ctg acc acc aag ttc		2715	
Ile Pro Pro Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe			
770	775	780	
aat gcc ttg att ggt ccg gag gct gaa cag gag aag cga gag aaa atg		2763	
Asn Ala Leu Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Glu Lys Met			
785	790	795	
gcc tca cca gct tac aca cca ctg acc acc aca gcc aaa gtc cgg cca		2811	
Ala Ser Pro Ala Tyr Thr Pro Leu Thr Thr Ala Lys Val Arg Pro			
800	805	810	
agg aaa cta gga ttt tca cac ttc gga aac ata aga aaa aag aag ttc		2859	
Arg Lys Leu Gly Phe Ser His Phe Gly Asn Ile Arg Lys Lys Lys Phe			
815	820	825	
gat gaa tcg acg gac tac att tgc cca atg gag ccc agt gac ggt gtc		2907	
Asp Glu Ser Thr Asp Tyr Ile Cys Pro Met Glu Pro Ser Asp Gly Val			
830	835	840	845
agt gat agt cac agg gtc tac agt ggc tac cgg ggc ctc agc ccc ctt		2955	
Ser Asp Ser His Arg Val Tyr Ser Gly Tyr Arg Gly Leu Ser Pro Leu			
850	855	860	
gat gcc cct gaa ctg gat ggg ctg gac cag gtg gga cag att agc tga		3003	
Asp Ala Pro Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser			
865	870	875	
tgcccttgtc acctgccctc tgtgcaccct gagagctcac agtaaacactg tgtgtgtcac		3063	

catataactg cacctcaccc ccgcacgtgt gcatgactcg cagagaatat tccagcaatt 3123
gtgtacccct gggccagtct cttaaaccc tgagggtggc caggatctgg agctgcac 3183
ctaaggggcc aggctttggg gaccattgcc aaaggtggac tcaggaggaa agacacttaa 3243
agacacttt acatgtctag taattcttga tgttcatctt cagcaccagt ggaaacacat 3303
gaacttcgat gcaggtccag agaccatgga cactcccacg aggctcagct ctcaggcacc 3363
ccctacactt cagttgaggg aaaagctcaa gtgccttagg cccgtggacc acagtcttgg 3423
ctgagatcaa agggatgagc aacagggact tctgccacag tgacaatgga attgtgttg 3483
gccttacttc agaggtggtc tcttcttct tgtaataaaa gcaatattta tgcgaaagc 3543

<210> 46
<211> 876
<212> PRT
<213> human

<400> 46

Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu Glu Gln Met
1 5 10 15

Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu Ser Asp Gly
20 25 30

Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met Asn Pro Phe
35 40 45

Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu Glu Met Leu
50 55 60

Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser Gln Ile Pro Gly Pro
65 70 75 80

Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu Glu Ser Leu Ser Gln Val
85 90 95

Asn His His Ser Ala Ala Ser Asn Glu Thr Tyr Gln Glu Arg Leu Ala
100 105 110

Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val Ser Val Leu
115 120 125

Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Val
130 135 140

Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu Glu Met Leu
145 150 155 160

Gln Gln Glu Leu Leu Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp
165 170 175

Leu Met Thr Glu Val Ser Glu Leu Lys Leu Lys Leu Val Gly Met Glu
180 185 190

Lys Glu Gln Arg Glu Gln Glu Lys Gln Arg Lys Ala Glu Glu Leu
195 200 205

Leu Gln Glu Leu Arg His Leu Lys Ile Lys Val Glu Glu Leu Glu Asn
210 215 220

Glu Arg Asn Gln Tyr Glu Trp Lys Leu Lys Ala Thr Lys Ala Glu Val
225 230 235 240

Ala Gln Leu Gln Glu Gln Val Ala Leu Lys Asp Ala Glu Ile Glu Arg
245 250 255

Leu His Ser Gln Leu Ser Arg Thr Ala Ala Leu His Ser Glu Ser His
260 265 270

Thr Glu Arg Asp Gln Glu Ile Gln Arg Leu Lys Met Gly Met Glu Thr
275 280 285

Leu Leu Leu Ala Asn Glu Asp Lys Asp Arg Arg Ile Glu Glu Leu Thr
290 295 300

Gly Leu Leu Asn Gln Tyr Arg Lys Val Lys Glu Ile Val Met Val Thr
305 310 315 320

Gln Gly Pro Ser Glu Arg Thr Leu Ser Ile Asn Glu Glu Glu Pro Glu
325 330 335

Gly Gly Phe Ser Lys Trp Asn Ala Thr Asn Lys Asp Pro Glu Glu Leu
340 345 350

Phe Lys Gln Glu Met Pro Pro Arg Cys Ser Ser Pro Thr Val Gly Pro
355 360 365

Pro Pro Leu Pro Gln Lys Ser Leu Glu Thr Arg Ala Gln Lys Lys Leu
370 375 380

Ser Cys Ser Leu Glu Asp Leu Arg Ser Glu Ser Val Asp Lys Cys Met
385 390 395 400

Asp Gly Asn Gln Pro Phe Pro Val Leu Glu Pro Lys Asp Ser Pro Phe
405 410 415

Leu Ala Glu His Lys Tyr Pro Thr Leu Pro Gly Lys Leu Ser Gly Ala
420 425 430

Thr Pro Asn Gly Glu Ala Ala Lys Ser Pro Pro Thr Ile Cys Gln Pro
435 440 445

Asp Ala Thr Gly Ser Ser Leu Leu Arg Leu Arg Asp Thr Glu Ser Gly
450 455 460

Trp Asp Asp Thr Ala Val Val Asn Asp Leu Ser Ser Thr Ser Ser Gly
465 470 475 480

Thr Glu Ser Gly Pro Gln Ser Pro Leu Thr Pro Asp Gly Lys Arg Asn
485 490 495

Pro Lys Gly Ile Lys Lys Phe Trp Gly Lys Ile Arg Arg Thr Gln Ser
500 505 510

Gly Asn Phe Tyr Thr Asp Thr Leu Gly Met Ala Glu Phe Arg Arg Gly
515 520 525

Gly Leu Arg Ala Thr Ala Gly Pro Arg Leu Ser Arg Thr Arg Asp Ser
530 535 540

Lys Gly Gln Lys Ser Asp Ala Asn Ala Pro Phe Ala Gln Trp Ser Thr
545 550 555 560

Glu Arg Val Cys Ala Trp Leu Glu Asp Phe Gly Leu Ala Gln Tyr Val
565 570 575

Ile Phe Ala Arg Gln Trp Val Ser Ser Gly His Thr Leu Leu Thr Ala
580 585 590

Thr Pro Gln Asp Met Glu Lys Glu Leu Gly Ile Lys His Pro Leu His
595 600 605

Arg Lys Lys Leu Val Leu Ala Val Lys Ala Ile Asn Thr Lys Gln Glu
610 615 620

Glu Lys Ser Ala Leu Leu Asp His Ile Trp Val Thr Arg Trp Leu Asp
625 630 635 640

Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu Ser Arg Val
645 650 655

Asp Arg Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu Leu Phe Leu
660 665 670

Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys Ala Ile His
675 680 685

Val Leu His Val Asn Lys Phe Asn Pro His Cys Leu His Arg Arg Pro
690 695 700

Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln Trp Ser Asn
705 710 715 720

His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala Glu Tyr Ala
725 730 735

Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile Ile Leu Glu
740 745 750

Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn Ile Pro Pro
755 760 765

Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe Asn Ala Leu
770 775 780

Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Glu Lys Met Ala Ser Pro
785 790 795 800

Ala Tyr Thr Pro Leu Thr Thr Ala Lys Val Arg Pro Arg Lys Leu
805 810 815

Gly Phe Ser His Phe Gly Asn Ile Arg Lys Lys Lys Phe Asp Glu Ser
820 825 830

Thr Asp Tyr Ile Cys Pro Met Glu Pro Ser Asp Gly Val Ser Asp Ser
835 840 845

His Arg Val Tyr Ser Gly Tyr Arg Gly Leu Ser Pro Leu Asp Ala Pro
850 855 860

Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser
865 870 875

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<211> 2819
<212> DNA
<213> human

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<221> CDS
<222> (77)..(1180)

<400> 47
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ccactgacgt ccaggc atg agg tgg ttc ctg ccc tgg acg ctg gca gca gtg 112
Met Arg Trp Phe Leu Pro Trp Thr Leu Ala Ala Val
1 5 10

aca gca gca gcc gcc agc acc gtc ctg gcc acg gcc ctc tct cca gcc 160
Thr Ala Ala Ala Ala Ser Thr Val Leu Ala Thr Ala Leu Ser Pro Ala
15 20 25

cct acg acc atg gac ttt acc cca gct cca ctg gag gac acc tcc tca 208
Pro Thr Thr Met Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser
30 35 40

cgc ccc caa ttc tgc aag tgg cca tgt gag tgc ccg cca tcc cca ccc 256
Arg Pro Gln Phe Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro
45 50 60

cgc tgc ccg ctg ggg gtc agc ctc atc aca gat ggc tgt gag tgc tgt 304
Arg Cys Pro Leu Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys
65 70 75

aag atg tgc gct cag cag ctt ggg gac aac tgc acg gag gct gcc atc 352
Lys Met Cys Ala Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile
80 85 90

tgt gac ccc cac cgg ggc ctc tac tgt gac tac agc ggg gac cgc ccg 400
Cys Asp Pro His Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro
95 100 105

agg tac gca ata gga gtg tgt gca cag gtg gtc ggt gtg ggc tgc gtc 448
Arg Tyr Ala Ile Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val
110 115 120

ctg gat ggg gtg cgc tac aac aac ggc cag tcc ttc cag cct aac tgc 496
Leu Asp Gly Val Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys
125 130 135 140

aag tac aac tgc acg tgc atc gac ggc gcg gtg ggc tgc aca cca ctg 544
Lys Tyr Asn Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu
145 150 155

tgc ctc cga gtg cgc ccc ccg cgt ctc tgg tgc ccc cac ccg cgg cgc 592
Cys Leu Arg Val Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg

160	165	170	
gtg agc ata cct ggc cac tgc tgt gag cag tgg gta tgt gag gac gac Val Ser Ile Pro Gly His Cys Cys Glu Gln Trp Val Cys Glu Asp Asp 175	180	185	640
gcc aag agg cca cgc aag acc gca ccc cgt gac aca gga gcc ttc gat Ala Lys Arg Pro Arg Lys Thr Ala Pro Arg Asp Thr Gly Ala Phe Asp 190	195	200	688
gct gtg ggt gag gtg gag gca tgg cac agg aac tgc ata gcc tac aca Ala Val Gly Glu Val Ala Trp His Arg Asn Cys Ile Ala Tyr Thr 205	210	215	736
agc ccc tgg agc cct tgc tcc acc agc tgc ggc ctg ggg gtc tcc act Ser Pro Trp Ser Pro Cys Ser Thr Ser Cys Gly Leu Gly Val Ser Thr 225	230	235	784
cgg atc tcc aat gtt aac gcc cag tgc tgg cct gag caa gag agc cgc Arg Ile Ser Asn Val Asn Ala Gln Cys Trp Pro Glu Gln Glu Ser Arg 240	245	250	832
ctc tgc aac ttg cgg cca tgc gat gtg gac atc cat aca ctc att aag Leu Cys Asn Leu Arg Pro Cys Asp Val Asp Ile His Thr Leu Ile Lys 255	260	265	880
gca ggg aag aag tgt ctg gct gtg tac cag cca gag gca tcc atg aac Ala Gly Lys Lys Cys Leu Ala Val Tyr Gln Pro Glu Ala Ser Met Asn 270	275	280	928
ttc aca ctt gcg ggc tgc atc agc aca cgc tcc tat caa ccc aag tac Phe Thr Leu Ala Gly Cys Ile Ser Thr Arg Ser Tyr Gln Pro Lys Tyr 285	290	295	976
tgt gga gtt tgc atg gac aat agg tgc tgc atc ccc tac aag tct aag Cys Gly Val Cys Met Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys 305	310	315	1024
act atc gac gtg tcc ttc cag tgt cct gat ggg ctt ggc ttc tcc cgc Thr Ile Asp Val Ser Phe Gln Cys Pro Asp Gly Leu Gly Phe Ser Arg 320	325	330	1072
cag gtc cta tgg att aat gcc tgc ttc tgt aac ctg agc tgt agg aat Gln Val Leu Trp Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn 335	340	345	1120
ccc aat gac atc ttt gct gac ttg gaa tcc tac cct gac ttc tca gaa Pro Asn Asp Ile Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Ser Glu 350	355	360	1168
att gcc aac tag gcaggcacaa atcttgggtc ttggggacta acccaatgcc Ile Ala Asn 365			1220
tgtgaaggcag tcagccctta tggccaataa cttttcacca atgagcctta gttaccctga			1280
tctggaccct tggcctccat ttctgtctct aaccattcaa atgacgcctg atggtgctgc			1340
tcaggcccat gctatgagtt ttctccttga tattcattcag catctactct aaagaaaaat			1400

gcctgtctct	agctgttctg	gactacaccc	aaggcctgatc	cagcctttcc	aagtcaactag	1460
aagtccctgct	ggatcttgcc	taaatcccaa	gaaatggaat	caggttagact	tttaatatca	1520
ctaatttctt	cttttagatgc	caaaccacaa	gactcttgg	gtccattcag	atgaatagat	1580
ggaatttggaa	acaatagaat	aatctattat	ttggagcctg	ccaagaggta	ctgtaatggg	1640
taattctgac	gtcagcgcac	caaaactatac	ctgattccaa	atatgtatgc	acctcaaggt	1700
catcaaacat	ttgccaagtg	agttgaatag	ttgcttaatt	ttgattttta	atggaaagtt	1760
gtatccatta	acctgggcat	tgtttagggtt	aagtttctct	tcaccctac	actgtgaagg	1820
gtacagatta	ggtttgtccc	agtcagaaat	aaaattttagt	aaacattcct	gttgatggga	1880
aaagccccca	gttaatactc	cagagacagg	gaaaggtcag	cccgtttcag	aaggaccaat	1940
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ccttgaatct	tctcccttgt	cctgcttggg	gttcatagga	attggtaagg	cctctggact	2060
ggcctgtctg	gccctgaga	gtgggtccct	ggaacactcc	tctactctta	cagagccttg	2120
agagacccag	ctgcagacca	tgccagaccc	actgaaatga	ccaagacagg	ttcaggttagg	2180
ggtgtgggtc	aaaccaagaa	gtgggtgccc	ttggtagcag	cctgggtga	cctctagagc	2240
tggaggctgt	gggactccag	gggccccgt	gttcaggaca	catctattgc	agagactcat	2300
ttcacagcct	ttcggtctgc	tgaccaaatg	gccagtttc	ttgttaggaag	atggaggttt	2360
accggttgtt	tagaaacaga	aatagactta	ataaaggaaa	aaagctgaag	agggtgaagc	2420
taaaaaggaaa	agggtgttgt	taatgaatat	caggctatta	tttattgtat	tagaaaata	2480
taatatttac	tgttagaatt	cttttatata	gggcctttc	tgtgccagac	attgctctca	2540
gtgcttgca	tgtattagct	cactgaatct	tcacgacaat	gttgagaagt	tcccattatt	2600
atttctgttc	ttacaaatgt	gaaacggaag	ctcatagagg	tgagaaaact	caaccagagt	2660
cacccagttg	gtgactggga	aagttaggat	tcagatcgaa	attggactgt	ctttataaacc	2720
catatttcc	ccctgtttt	agagcttcca	aatgtgtcag	aataggaaaa	cattgcaata	2780
aatggcttga	ttttttaaaa	aaaaaaaaaa	aaaaaaaaaa			2819

<210> 48
 <211> 367
 <212> PRT
 <213> human

 <400> 48

Met Arg Trp Phe Leu Pro Trp Thr Leu Ala Ala Val Thr Ala Ala Ala
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Ala Ser Thr Val Leu Ala Thr Ala Leu Ser Pro Ala Pro Thr Thr Met
20 25 30

Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser Arg Pro Gln Phe
35 40 45

Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro Arg Cys Pro Leu
50 55 60

Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Met Cys Ala
65 70 75 80

Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
85 90 95

Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
100 105 110

Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
115 120 125

Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys Lys Tyr Asn Cys
130 135 140

Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu Cys Leu Arg Val
145 150 155 160

Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg Val Ser Ile Pro
165 170 175

Gly His Cys Cys Glu Gln Trp Val Cys Glu Asp Asp Ala Lys Arg Pro
180 185 190

Arg Lys Thr Ala Pro Arg Asp Thr Gly Ala Phe Asp Ala Val Gly Glu
195 200 205

Val Glu Ala Trp His Arg Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
210 215 220

Pro Cys Ser Thr Ser Cys Gly Leu Gly Val Ser Thr Arg Ile Ser Asn
225 230 235 240

Val Asn Ala Gln Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
245 250 255

Arg Pro Cys Asp Val Asp Ile His Thr Leu Ile Lys Ala Gly Lys Lys
260 265 270

Cys Leu Ala Val Tyr Gln Pro Glu Ala Ser Met Asn Phe Thr Leu Ala
275 280 285

Gly Cys Ile Ser Thr Arg Ser Tyr Gln Pro Lys Tyr Cys Gly Val Cys
290 295 300

Met Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Asp Val
305 310 315 320

Ser Phe Gln Cys Pro Asp Gly Leu Gly Phe Ser Arg Gln Val Leu Trp
325 330 335

Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
340 345 350

Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Ser Glu Ile Ala Asn
355 360 365

<210> 49
<211> 1768
<212> DNA
<213> human

<220>
<221> CDS
<222> (356) .. (868)

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ggacctggag tggcaactggg cgcggacgg accatccccg ggaccgcct gcccctcggc 120
gccccgcccc gccgggcccgc tccccgtcgg gttccccagc cacagcctta cctacgggct 180
cctgactccg caaggcttcc agaagatgct cgaaccacccg gccggggcct cggggcagca 240
gtgagggagg cgtccagccc cccactcagc tcttctcctc ctgtgccagg ggctccccgg 300
gggatgagca tggtggtttt ccctcgagc cccctggctc gggacgtctg agaag atg
Met 1

ccg gtc atg agg ctg ttc cct tgc ttc ctg cag ctc ctg gcc ggg ctg 406
Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly Leu
5 10 15

gcg ctg cct gct gtg ccc ccc cag cag tgg gcc ttg tct gct ggg aac 454
Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly Asn
20 25 30

ggc tcg tca gag gtg gaa gtg gta ccc ttc cag gaa gtg tgg ggc cgc	502
Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly Arg	
35 40 45	
agc tac tgc cgg gcg ctg gag agg ctg gtg gac gtc gtg tcc gag tac	550
Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu Tyr	
50 55 60 65	
ccc agc gag gtg gag cac atg ttc agc cca tcc tgt gtc tcc ctg ctg	598
Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu Leu	
70 75 80	
cgc tgc acc ggc tgc tgc ggc gat gag aat ctg cac tgt gtg ccg gtg	646
Arg Cys Thr Gly Cys Gly Asp Glu Asn Leu His Cys Val Pro Val	
85 90 95	
gag acg gcc aat gtc acc atg cag ctc cta aag atc cgt tct ggg gac	694
Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly Asp	
100 105 110	
cgg ccc tcc tac gtg gag ctg acg ttc tct cag cac gtt cgc tgc gaa	742
Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys Glu	
115 120 125	
tgc cgg cct ctg cgg gag aag atg aag ccg gaa agg agg aga ccc aag	790
Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro Lys	
130 135 140 145	
ggc agg ggg aag agg agg aga gag aag cag aga ccc aca gac tgc cac	838
Gly Arg Gly Lys Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys His	
150 155 160	
ctg tgc ggc gat gct gtt ccc cgg agg taa cccacccctt ggaggagaga	888
Leu Cys Gly Asp Ala Val Pro Arg Arg	
165 170	
gaccggcac ccggctcgta tatttattac cgtcacactc ttcatgtact cctgctggta	948
cctgccccctt atttatttagc caactgtttc cctgctgaat gcctcgctcc cttcaagacg	1008
agggggcaggg aaggacagga ccctcaggaa ttcatgtgc tcaacaacgt gagagaaaga	1068
gagaagccag ccacagaccc ctgggagtt ccgccttgaa agaagcaaga cacgtggcct	1128
cgtgaggggc aagctaggcc ccagaggccc tggaggtctc cagggccctg cagaaggaaa	1188
gaagggggcc ctgctacctg ttcttggcc tcaggctctg cacagtcaag cagcccttgc	1248
tttcggagct cctgtccaaa agtagggatg cggatcctgc tggggccgcc acggcctggc	1308
tggtggaag gccggcagcg ggcggagggg atccagccac ttccccctct tcttctgaag	1368
atcagaacat tcagctctgg agaacagtgg ttgcctgggg gctttgcca ctccttgtcc	1428
cccgatct cccctcacac tttgccattt gcttgtactg ggacattgtt cttccggcc	1488
aaggtgccac caccctgccc cccctaagag acacatacag agtggggccc gggctggaga	1548
aagagctgcc tggatgagaa acagctcagc cagtggggat gaggtcacca ggggaggagc	1608

ctgtgcgtcc cagctgaagg cagtggcagg ggagcagggtt ccccaagggc cctggcaccc 1668
ccacaagctg tccctgcagg gccatctgac tgccaagcca gattctcttg aataaaagtat 1728
tctagtgtgg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1768

<210> 50
<211> 170
<212> PRT
<213> human

<400> 50

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro
130 135 140

Lys Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys
145 150 155 160

His Leu Cys Gly Asp Ala Val Pro Arg Arg
165 170

<210> 51

<211> 3874
 <212> DNA
 <213> human

 <220>
 <221> CDS
 <222> (1)..(1902)

 <400> 51
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 Met Ala His Leu Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr
 1 5 10 15

 cat aaa aag ttc tgg aag ctt ggt gca gta att ttt ttc ttt ata ata 96
 His Lys Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Ile Ile
 20 25 30

 gtt ttg gtt tta atg caa aga gaa gta agt gtt caa tat tcc aaa gag 144
 Val Leu Val Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
 35 40 45

 gaa tca agg atg gaa agg aac atg aaa aac aaa aac aag atg ttg gat 192
 Glu Ser Arg Met Glu Arg Asn Met Lys Asn Lys Asn Lys Met Leu Asp
 50 55 60

 tta atg cta gaa gct gta aac aat att aag gat gcc atg cca aaa atg 240
 Leu Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
 65 70 75 80

 caa ata gga gca cct gtc agg caa aac att gat gct ggt gag aga cct 288
 Gln Ile Gly Ala Pro Val Arg Gln Asn Ile Asp Ala Gly Glu Arg Pro
 85 90 95

 tgt ttg caa gga tat tat aca gca gca gaa ttg aag cct gtc ctt gac 336
 Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Leu Asp
 100 105 110

 cgt cca cct cag gat tca aat gca cct ggt gct tct ggt aaa gca ttc 384
 Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Ala Phe
 115 120 125

 aag aca acc aat tta agt gtt gaa gag caa aag gaa aag gaa cgt ggg 432
 Lys Thr Thr Asn Leu Ser Val Glu Glu Gln Lys Glu Lys Glu Arg Gly
 130 135 140

 gaa gct aaa cac tgc ttt aat gct ttc gca agt gac agg att tct ttg 480
 Glu Ala Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
 145 150 155 160

 cac cga gat ctt gga cca gac act cga cct cct gaa tgt att gaa caa 528
 His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
 165 170 175

 aaa ttt aag cgc tgc cct ccc ctg ccc acc acc agt gtc ata ata gtt 576
 Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
 180 185 190

 ttt cat aat gaa gcg tgg tcc acg ttg ctt aga act gtc cac agt gtg 624
 Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val

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gat gct agt gta gat gag tac tta cat gat aaa cta gat gaa tat gta Asp Ala Ser Val Asp Glu Tyr Leu His Asp Lys Leu Asp Glu Tyr Val 225	230	235	720
aaa caa ttt tct ata gta aaa ata gtc aga caa aga gaa aga aaa ggt Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Arg Glu Arg Lys Gly 245	250	255	768
ctg atc act gct cgg ttg cta gga gca aca gtc gca aca gct gaa acg Leu Ile Thr Ala Arg Leu Leu Gly Ala Thr Val Ala Thr Ala Glu Thr 260	265	270	816
ctc aca ttt tta gat gct cac tgt gag tgt ttc tat ggt tgg cta gaa Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu 275	280	285	864
cct ctg ttg gcc aga ata gct gag aac tac acg gct gtc gta agt cca Pro Leu Leu Ala Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro 290	295	300	912
gat att gca tcc ata gat ctg aac acg ttt gaa ttc aac aaa cct tct Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser 305	310	315	960
cct tat gga agt aac cat aac cgt gga aat ttt gac tgg agt ctt tca Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser 325	330	335	1008
ttt ggc tgg gag tcg ctt cct gat cat gag aag caa aga agg aaa gat Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp 340	345	350	1056
gaa acc tac cca att aaa aca ccc act ttt gca gga gga ctt ttt tcc Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser 355	360	365	1104
ata tca aaa gaa tat ttt gag tat att gga agc tat gat gaa gaa atg Ile Ser Lys Glu Tyr Phe Glu Tyr Ile Gly Ser Tyr Asp Glu Glu Met 370	375	380	1152
gaa atc tgg gga ggt gaa aat ata gaa atg tct ttc aga gta tgg caa Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln 385	390	395	1200
tgt ggt ggg cag ttg gag att atg cct tgc tct gtt gtt gga cat gtt Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val 405	410	415	1248
ttt cgc agc aaa agc cct cat agc ttt cca aaa ggc act cag gtg att Phe Arg Ser Lys Ser Pro His Ser Phe Pro Lys Gly Thr Gln Val Ile 420	425	430	1296
gct aga aac caa gtt cgc ctt gca gaa gtc tgg atg gat gaa tac aag Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys			1344

435	440	445	
gaa ata ttt tat agg aga aat aca gat gca gca aaa att gtt aaa caa Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln 450	455	460	1392
aaa gca ttt ggt gat ctt tca aaa aga ttt gaa ata aaa cac cgt ctt Lys Ala Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys His Arg Leu 465	470	475	1440
cgg tgt aaa aat ttt aca tgg tat ctg aac aac att tat cca gag gtg Arg Cys Lys Asn Phe Thr Trp Tyr Leu Asn Asn Ile Tyr Pro Glu Val 485	490	495	1488
tat gtg cca gac ctt aat cct gtt ata tct gga tac att aaa agc gtt Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val 500	505	510	1536
ggt cag cct cta tgt ctg gat gtt gga gaa aac aat caa gga ggc aaa Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys 515	520	525	1584
cca tta att atg tat aca tgt cat gga ctt ggg gga aac cag tac ttt Pro Leu Ile Met Tyr Thr Cys His Gly Leu Gly Asn Gln Tyr Phe 530	535	540	1632
gaa tac tct gct caa cat gaa att cgg cac aac atc cag aag gaa tta Glu Tyr Ser Ala Gln His Glu Ile Arg His Asn Ile Gln Lys Glu Leu 545	550	555	1680
tgt ctt cat gct caa ggt ctc gtt cag ctg aag gca tgt acc tac Cys Leu His Ala Ala Gln Gly Leu Val Gln Leu Lys Ala Cys Thr Tyr 565	570	575	1728
aaa ggt cac aag aca gtt gtc act gga gag cag ata tgg gag atc cag Lys Gly His Lys Thr Val Val Thr Gly Glu Gln Ile Trp Glu Ile Gln 580	585	590	1776
aag gat caa ctt cta tac aat cca ttc tta aaa atg tgc ctt tca gca Lys Asp Gln Leu Leu Tyr Asn Pro Phe Leu Lys Met Cys Leu Ser Ala 595	600	605	1824
aat gga gag cat cca agt tta gtg tca tgc aac cca tca gat cca ctc Asn Gly Glu His Pro Ser Leu Val Ser Cys Asn Pro Ser Asp Pro Leu 610	615	620	1872
caa aaa tgg ata ctt agc caa aat gat taa gtgttcctta aaatataagtt Gln Lys Trp Ile Leu Ser Gln Asn Asp 625	630		1922
aaaaaaaggaa atatttttc tcataaaaact gtgacttaggc atacactgta gtttttgaaa attatgcataa agcagctaaa tgtaacttat tccaaagtgc tttttcttat ttatatcttt atgttagcact actacagaaa ttctgcaagt ttctgtttca aagcacaata actagtaata ccaaagacta tttcaaaaatg tccagatgta gggaaagaga tgtttacagt atgatgaaaa taatttcca agtaaagtga tgtttgttg ttttgtacac ttagggatat atatatata 640	645	650	1982
			2042
			2102
			2162
			2222

ctacattcac acactcacaa tttaaaatat ttcccctagt ttttgggg gataggaaga	2282
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gaacttttt ttgcgttgg tttacttgc tgtcaaatgt ttccttaaac atgaaactga	2462
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gatactgtgt gtttcccaa agcactttt aaaaaatttt tataaattac tatctgttga	2642
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His Lys Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Ile Ile
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Val Leu Val Leu Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
35 40 45

Glu Ser Arg Met Glu Arg Asn Met Lys Asn Lys Asn Lys Met Leu Asp
50 55 60

Leu Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
65 70 75 80

Gln Ile Gly Ala Pro Val Arg Gln Asn Ile Asp Ala Gly Glu Arg Pro
85 90 95

Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Leu Asp
100 105 110

Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Ala Phe
115 120 125

Lys Thr Thr Asn Leu Ser Val Glu Glu Gln Lys Glu Lys Glu Arg Gly
130 135 140

Glu Ala Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
145 150 155 160

His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
165 170 175

Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
180 185 190

Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val
195 200 205

Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp
210 215 220

Asp Ala Ser Val Asp Glu Tyr Leu His Asp Lys Leu Asp Glu Tyr Val
225 230 235 240

Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Arg Glu Arg Lys Gly
245 250 255

Leu Ile Thr Ala Arg Leu Leu Gly Ala Thr Val Ala Thr Ala Glu Thr
260 265 270

Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu
275 280 285

Pro Leu Leu Ala Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro
290 295 300

Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser
305 310 315 320

Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser
325 330 335

Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp
340 345 350

Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser
355 360 365

Ile Ser Lys Glu Tyr Phe Glu Tyr Ile Gly Ser Tyr Asp Glu Glu Met
370 375 380

Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln
385 390 395 400

Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val
405 410 415

Phe Arg Ser Lys Ser Pro His Ser Phe Pro Lys Gly Thr Gln Val Ile
420 425 430

Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys
435 440 445

Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln
450 455 460

Lys Ala Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys His Arg Leu
465 470 475 480

Arg Cys Lys Asn Phe Thr Trp Tyr Leu Asn Asn Ile Tyr Pro Glu Val
485 490 495

Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val
500 505 510

Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys
515 520 525

Pro Leu Ile Met Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe
530 535 540

Glu Tyr Ser Ala Gln His Glu Ile Arg His Asn Ile Gln Lys Glu Leu
545 550 555 560

Cys Leu His Ala Ala Gln Gly Leu Val Gln Leu Lys Ala Cys Thr Tyr
565 570 575

Lys Gly His Lys Thr Val Val Thr Gly Glu Gln Ile Trp Glu Ile Gln
580 585 590

Lys Asp Gln Leu Leu Tyr Asn Pro Phe Leu Lys Met Cys Leu Ser Ala
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